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<p>(21) International Application Number: PCT/US98/04493</p> <p>(22) International Filing Date: 6 March 1998 (06.03.98)</p> <p>(30) Priority Data:</p> <table border="0"> <tr><td>60/040,162</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,333</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/038,621</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,161</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,626</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,334</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,336</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,163</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/043,580</td><td>11 April 1997 (11.04.97)</td><td>US</td></tr> <tr><td>60/043,568</td><td>11 April 1997 (11.04.97)</td><td>US</td></tr> </table> <p><i>(Continued on the following page)</i></p> <p>(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).</p> <p>(72) Inventors; and</p> <p>(75) Inventors/Applicants (for US only): RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hills Road, Laytonsville, MD 20882 (US). FISCHER, Carrie, L. [US/US]; 5810 Hall Street, Burke, VA 22015 (US). SOPPETH, Daniel, R. [US/US]; 15050 Stillfield, Place, Centreville, VA 22020 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US). BEDNARIK, Daniel, P. [US/US]; 8822 Blue Sea Drive, Columbia, MD 21046 (US). ENDRESS, Gregory, A. [US/US]; 9729 Clagett Farm Drive, Potomac, MD 20854 (US). YU, Guo-Liang [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). FENG, Ping [CN/US]; 4 Relda Court, Gaithersburg, MD 20878 (US). YOUNG, Paul, E. [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 13203 L Astoria Hill Court, Germantown,</p>		60/040,162	7 March 1997 (07.03.97)	US	60/040,333	7 March 1997 (07.03.97)	US	60/038,621	7 March 1997 (07.03.97)	US	60/040,161	7 March 1997 (07.03.97)	US	60/040,626	7 March 1997 (07.03.97)	US	60/040,334	7 March 1997 (07.03.97)	US	60/040,336	7 March 1997 (07.03.97)	US	60/040,163	7 March 1997 (07.03.97)	US	60/043,580	11 April 1997 (11.04.97)	US	60/043,568	11 April 1997 (11.04.97)	US	<p>MD 20874 (US). DUAN, Roxanne [US/US]; 4541 Fairfield Drive, Bethesda, MD 20814 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). FLORENCE, Kimberly, A. [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316, Gaithersburg, MD 20878 (US). BREWER, Laurie, A. [US/US]; 14920 Mount Nebo Road, Poolesville, MD 20837 (US). MOORE, Paul, A. [GB/US]; Apartment #104, 1908 Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yanggu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W. #807, Washington, DC 20009 (US). LI, Yi [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). ZENG, Zhizhen [CN/US]; 13950 Saddleview Drive, Gaithersburg, MD 20878 (US). KYAW, Hla [BU/US]; 520 Sugarbush Circle, Frederick, MD 21703 (US).</p> <p>(74) Agents: BROOKES, Anders, A. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published</p> <p><i>Without international search report and to be republished upon receipt of that report.</i></p> <p><i>With an indications in relation to deposited biological material furnished under Rule 13^{bis} separately from the description.</i></p>
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<p>(54) Title: 186 HUMAN SECRETED PROTEINS</p> <p>(57) Abstract</p> <p>The present invention relates to 186 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>																																

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186 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and
5 their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or
10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum
15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

20 Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or
25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include
30 the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using
35 secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 12301 Park Lawn Drive, Rockville, Maryland 20852, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA contained within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and
10 double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS -
5 STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990);
10 Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting
15 activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present
20 invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

25 **Polynucleotides and Polypeptides of the Invention**

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

This gene is expressed primarily in testes tumor and to a lesser extent in fetal brain.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly of the testes, and defects of the central nervous system such as seizure and neurodegenerative disorders. Similarly, polypeptides and antibodies
35 directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly cancer of the testes and central nervous system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testes and other reproductive tissue, brain and other tissue of the nervous system, and blood cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of testicular cancer and treatment of central nervous system disorders since this gene is primarily expressed in the testes tumor and developing brain.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

This gene is expressed primarily in cancer tissues, such as breast cancer and Wilm's tumor, and to a lesser extent in fetal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and/or tumors, particularly, those found in the breast, and developmental abnormalities or disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the glandular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, and fetal tissue and, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 314 as residues: Pro-11 to Thr-18, Leu-43 to Pro-50, Gly-64 to Leu-72, and Leu-81 to Lys-86.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of cancers and/or tumors, particularly, those found in the breast since expression is mainly in cancer/tumor tissues. May serve as therapeutic proteins for proliferation/differentiation of fetal tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

This gene is expressed primarily in CD34 depleted buffy coat and to a lesser extent in spleen, chronic lymphocytic leukemia.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood disorders or leukemias, diseases of the immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
- 10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
- 15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders or
- 20 leukemias, diseases of the immune system since expression is in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene is expressed primarily in CD34 depleted buffy coat.

- 25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood disorders or lymphocytic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
- 30 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
- 35 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders since expression is in tissues related to immune function.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 5

This gene is expressed primarily in CD34 depleted buffy coat.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood or immune
10 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous
15 and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 317 as residues:
20 Pro-13 to Lys-21.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders since expression is in tissues related to immune function.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 6

This gene is expressed primarily in CD34 depleted buffy coat.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood or immune
30 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., and blood cells, and
35 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level

in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 318 as residues: Lys-31 to Lys-39.

- 5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood diseases since it is expressed in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

- 10 This gene is expressed primarily in CD34 depleted buffy coat and to a lesser extent in pineal gland.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases of the immune system and brain associated diseases. Similarly, polypeptides and antibodies directed to
15 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and pineal gland, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 25 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders, immune diseases or brain associated diseases (specifically of the pineal gland) since expression is in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

- 30 The translation product of this gene shares sequence homology with an organic cation transporter which is thought to be important in organic cation uptake in the kidney and liver. (See Accession No. 2343059.) Preferred polypeptide fragments comprise the amino acid sequence ITIAIQMICLVNXELYPTFVRNXGVMVCSSLCDIGGIPT
FIVFRLREVWQALPLILFAVLGLLAAGVTLLLPETKGVLPETMKDAENLGRKAKPKENTIYLK
35 VQTSEPSGT (SEQ ID NO: 615) or TMKDAENLGRKAKPKENT (SEQ ID NO: 616) as well as N-terminal and C-terminal deletions of these fragments. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatic and renal diseases where drug elimination/cation exchange (organic cation uptake) in the liver and kidney are problematic. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic or renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 320 as residues: Asn-64 to Asn-74, and Gln-81 to Gly-87.

The tissue distribution and homology to organic cation transporter indicate that polynucleotides and polypeptides corresponding to this gene are useful as a polyspecific transporter that is important for drug elimination in the liver (and possibly kidney) since expression is found in the liver.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This gene is expressed primarily in eosinophil induced with IL-5 and to a lesser extent in fetal liver and spleen. This gene also maps to chromosome 15, and therefore can be used in linkage analysis as a marker for chromosome 15.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases of the immune system, particularly allergies or asthma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the

standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/diagnosis of diseases involving eosinophil reactions since expression seems to be concentrated in eosinophils and other tissues involved in immunity such as the liver and spleen.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in tissues of hematopoietic lineage and to a lesser extent in Hodgkins lymphoma. Any frame shifts in this sequence can easily be clarified using known molecular biology techniques.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and immune deficiency or dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, lymphoid and reticuloendothelial tissues, and cancerous tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/ diagnosis for lymphomas or immune dysfunction or as a therapeutic protein useful in immune modulation based on expression in anergic T-cells and lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in neutrophils and to a lesser extent in activated lymphoid cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the cell type present in a biological sample and for diagnosis of diseases and conditions: inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
5 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 323 as residues: Glu-40 to Lys-46.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for modulation of an immune reaction or as a growth factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

15 This gene is expressed primarily in brain and to a lesser extent in activated T-cells. It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. Preferred polypeptide fragments comprise the amino acid sequence PRVRNSPEDLGLSLTGDSCKL (SEQ ID NO:617).

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurodegenerative disorders including ischemic shock, alzheimers and cognitive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
25 number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and brain, and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
30 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 324 as residues: Ser-5 to Glu-14, Ile-21 to Pro-35, Ser-65 to Asp-81, Cys-89 to Val-96, Lys-136 to Ser-145, Ile-152 to Met-169, and Arg-189 to Lys-196.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnostic/treatment for cancers of the given tissue or in the treatment of neurological disorders of the CNS.

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

This gene was also recently cloned by other groups, naming this calcium-activated potassium channel gene, hKCa4. (See Accession No. AF033021, see also, Accession No. 2584866.) This gene is mapped to human chromosome 19q13.2. A second signal sequence likely exists upstream from the predicted signal sequence as described in Table 1. Preferred polypeptide fragments comprise: QADDLQATVAALCVLRGGGPWAG SWLSPKTPGAMGGDLVLGLGALRRRKRL (SEQ NO: 618); or EQEKSLAGWALVLAXXGIGL MVLHAEMLWFGGCSAVNATGHLSDTLWLIPITFLTIGYGDVVPGTMWGKIVCLCTGVMGVCC TALLVAVVARKLEFNKAIEKHVHNFMMDIQYTKEMKESAAARVLQEAWMFYKHTRRKESHAAR XHQRXLLAAINAFRQVRLKHKRLREQVNSMVDISKMHMILYDLQQNLSSSHRALEKQIDTLAG KLDALTELLSTALGPRQLPEPSQQSK (SEQ ID NO: 619), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in breast lymph node and T-cells, and to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hematologic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lymphoid tissue, blood cells and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 325 as residues: Arg-13 to Lys-23.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment/diagnosis of hematologic and diseases involving immune modulation based on distribution in the lymph node and T-cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

This gene was recently cloned by another group, calling it PAPS synthase. (See Accession No. e1204135.) Preferred polypeptide fragments comprise the amino acid sequence YQAHHVS RNKRGQVVGTRGGFRGCTVWLTGLSGAGK (SEQ ID NO: 620).

5 Also preferred are the polynucleotide fragments encoding this polypeptide fragment.

It has been discovered that this gene is expressed primarily in benign prostate hyperplasia, Human Umbilical Vein Endothelial Cells and to a lesser extent in smooth muscle and Human endometrial stromal cells-treated with estradiol.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammation, ischemia, and restenosis, based on endothelial cell and smooth muscle cell expression, and prostate diseases such as benign prostate hyperplasia or prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate or vessels of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate, endothelial cells, smooth muscle, and endometrium, and cancerous and wounded tissues) or bodily
20 fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 326 as residues: Arg-21 to Asp-26, Lys-35 to Lys-44,
25 Glu-49 to Asn-58.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/diagnosing diseases or conditions where the endothelial cell lining of the veins and arteries of underlying smooth muscle are involved.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 15

This gene is expressed primarily in human 6 week embryo and to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: developmental anomalies or fetal deficiencies. Similarly, polypeptides and antibodies directed to these

polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly developmental in nature, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 327 as residues Lys-50 to Glu-57.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection of developmental abnormalities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

This gene is expressed primarily in kidney and amygdala and to a lesser extent in fetal tissues. This gene is mapped to chromosome 14, and therefore is useful in linkage analysis as a marker for chromosome 14.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) present in a biological sample and for diagnosis of diseases and conditions: kidney diseases, neurological disorders and developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s). For a number of disorders of the above tissues, particularly of the renal system or developing fetal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, amygdala, and fetal tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of conditions affecting the brain, kidneys and fetal development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 17

This gene is expressed primarily in ovarian cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: solid tumors similar to ovarian cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovarian and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 329 as residues Ser-51 to Val-56.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of solid tumors of the reproductive system such as ovarian cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

This gene is expressed primarily in brain medulloblastoma. Preferred polypeptide fragments comprise the amino acid sequence: IRHEQHPNFSLEMHSGSSLLFLPQL ILILPVCAHLHEELNC (SEQ ID NO: 643) and SFFISEEKGHLLLQAERHPWVAGALVGVSGLTTLTCSGPTEKPATKNYFLKRLQEMHIRAN (SEQ ID NO: 644), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors particularly of the CNS or. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating medulloblastoma or similar tumors.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 19

This gene is expressed primarily in adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adipose tissues expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipocytes and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating obesity by regulating the function and number of adipocytes

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

This gene is expressed primarily in B cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of the immune system with an emphasis on B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tumors of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of B cell derived
5 tumors based on its expression in b cell lymphomas

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

This gene is expressed primarily in immune cells and to a lesser extent in fetal tissues

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
15 type(s). For a number of disorders of the above tissues or cells, particularly of the immune expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cells of the immune system, and fetal tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
20 individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:333 as residues Asp-10 to Pro-19, Ser-74 to Tyr-79, Glu-95 to Lys-110.

The tissue distribution indicates that polynucleotides and polypeptides
25 corresponding to this gene are useful for treatment of diseases involving alterations in T cell activity.

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

It has been discovered that this gene is expressed primarily in ovarian tumor.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors particularly of the ovary. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
35 or cell type(s). For a number of disorders of the above tissues or cells, particularly of tumors of the reproductive organs, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovarian

and other reproductive tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 334 as residues: Leu-22 to Gln-27.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of ovarian tumors as it has only been identified in ovarian tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 23

It has been discovered that this gene is expressed primarily in fetal tissues and to a lesser extent in osteoclastoma cell line

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: osteoporosis or arthritis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone cells, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of conditions of abnormal bone remodeling due to enhanced activity of osteoclasts. This may be useful as a specific marker for malignancies derived from osteoclasts or their precursors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The translation product of this gene shares sequence homology with a periplasmic ribonuclease which is thought to be important in degrading extracellular polynucleotides

It has been discovered that this gene is expressed primarily in serum treated smooth muscle cells

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: vascular disease such as restenosis. Similarly, polypeptides and antibodies directed to these polypeptides are
5 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculature expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
10 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 336 as residues: Gln-30 to Lys-36, and Pro-41 to Arg-48.

15 The tissue distribution and homology to ribonucleases indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of pathological conditions of smooth muscle associated with bacterial or viral infiltration

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

20 This gene is expressed primarily in Early Stage Human Brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: human brain development and related diseases. Similarly, polypeptides and antibodies directed to
25 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain development and related diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and
30 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to this gene indicate that polynucleotides
35 and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases affecting human brain development and related diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

It has been discovered that this gene is expressed primarily in human brain tissue.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: human brain diseases and other diseases related to brain diseases, which may be caused by brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
- 10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
- 15 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution and homology to the gene indicate that polynucleotides
- 20 and polypeptides corresponding to this gene are useful for diagnosis and treatment of human brain diseases and other diseases related.

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

It has been discovered that this gene is expressed primarily in Anergic T-cells.

- 25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune diseases, inflammatory diseases and diseases related to T lymph cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological
- 30 probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune diseases, inflammatory diseases and diseases related to T lymph cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g.,
- 35 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for immune diseases,
5 inflammatory diseases and diseases related to T lymph cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 28

- The translation product of this gene shares sequence homology with *Shigella flexneri* positive transcriptional regulator CriR (criR) gene which is thought to be
10 important in regulation of gene expression.

This gene is expressed primarily in human synovial sarcoma and normal human brain tissues.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions: human brain diseases particularly sarcomas of the synovium. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain and synovium and other related human
20 brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., synovial tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
25 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of human synovial sarcoma and other related human brain diseases.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed in bone marrow, infant brain, fetal liver and spleen, prostate and to a lesser extent in pineal gland, adipose tissue, kidney, adrenal gland, umbilical vein endothelial cells, and T cells.

- 35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases related to bone marrow or

hematopoietic tissues, prostate, kidney, adrenal gland, and cardiovascular tissue or organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases related to hematopoietic tissues, immune system, prostate, kidney, adrenal gland, and cardiovascular tissue or organs, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, hematopoietic cells, pineal gland, adipose tissue, kidney, adrenal gland, endothelial cells, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases related to hematopoietic tissues, immune system, prostate, kidney, adrenal gland, and cardiovascular tissue or organs.

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

This gene is expressed primarily in meningea and to a lesser extent in breast and adult brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Diseases of the meningea and related brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the meningea and related brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., meningea, mammary tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the meningea and related brain diseases.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 31**

This gene is expressed in meningea, fetal spleen, osteoblast and to a lesser extent in activated T-cells, endometrial stromal cells, fetal lung, HL-60, thymus, testis and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: meningeal disease, osteoporosis, immune diseases, and hematoplastic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell type(s). For a number of disorders of the
15 above tissues or cells, particularly of the meningeal diseases, osteoporosis, immune diseases, and hematoplastic diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, endometrium, lung, thymus, testis, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of
25 meningeal, osteoporosis, immune diseases, hematoplastic diseases, testis diseases and lung diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

This gene is expressed primarily in human thymus and to a much lesser extent
30 in infant brain, T-cells, smooth muscle, endothelial cells, bone marrow, human ovarian tumor and keratinocytes testes, osteoclastoma, breast, and tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Diseases involving the
35 thymus, particularly thymic cancer and diseases involving T-cell maturation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a

number of disorders of the above tissues or cells, particularly of the thymus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., thymus, brain, and other tissue of the nervous system, blood cells, bone marrow, ovaries, and testes, and other reproductive tissue, mammary
5 tissue, tonsils, melanocytes and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution and homology to gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the thymus particularly thymic cancer and diseases involving T-cell maturation.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 33**

This gene is expressed primarily in human tonsils, and placenta, and to a lesser extent in adipocytes, melanocyte, and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammatory diseases, immune diseases, and obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the inflammatory diseases, immune diseases, and obesity, expression of
25 this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., tonsils, placenta, adipocytes, melanocytes, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
30 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to this gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases such as inflammation, immune diseases, and obesity.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene is expressed in activated T cells, and to a lesser extent in pituitary, testis, and breast lymph node.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases relating to T cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the disorders of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pituitary, testes and other reproductive tissue, mammary tissue, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of immune disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 35

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases relating to neurological disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain, and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: neurological disorders.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
type(s). For a number of disorders of the above tissues or cells, particularly of the
10 diseases relating to neurological disorders, expression of this gene at significantly
higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,
brain and other tissue of the nervous system, and cancerous and wounded tissues) or
bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
tissue or cell sample taken from an individual having such a disorder, relative to the
15 standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of neurological
disorders.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

This gene is expressed primarily in human ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions: ovarian cancer.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
type(s). For a number of disorders of the above tissues or cells, particularly of the
ovarian disorders such as those involving germ cells, ovarian follicles, stromal cells,
30 expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., ovary and other reproductive tissue, and
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
35 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of ovarioopathy.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

This gene is expressed primarily in lymph node breast cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: breast cancer. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
number of disorders of the above tissues or cells, particularly of the breast cancer,
10 expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., mammary tissue and lymphoid tissue, and
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
15 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for used as a diagnostic marker for breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

20 This gene is expressed primarily in brain and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: neuronal disorders such
as trauma, brain degeneration, and brain tumor. Similarly, polypeptides and antibodies
25 directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the brain, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., brain and other tissue of the nervous system, and cancerous and wounded
30 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
35 corresponding to this gene are useful for diagnosis and therapeutic treatment of
neuronal disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 40

This gene is expressed in early stage human embryo, adrenal gland tumor, and
5 immune tissues such as fetal liver, fetal spleen, T-cell, and myeloid progenitor cell line
and to a lesser extent in ovary, colon cancer, and a few other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: tumorigenesis including
10 adrenal gland tumor, colon cancer and various other tumors, developmental and
immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides
are useful in providing immunological probes for differential identification of the
tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the cancer tissues, early stage human tissues, and immune system,
15 expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., liver, spleen, blood cells, bone marrow, ovary
and other reproductive tissue, and colon, and cancerous and wounded tissues) or bodily
fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
cell sample taken from an individual having such a disorder, relative to the standard
20 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and therapeutic treatment of immune
and developmental disorders, and tumorigenesis.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene is expressed primarily in fetal lung, endothelial cells, liver, thymus
and a few other immune tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: immune disorders such
as immune deficiency and autoimmune diseases, pulmonary diseases, liver diseases,
and tumor matasis. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
35 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the fetal lung, liver, endothelial cells, and immune tissues, expression of
this gene at significantly higher or lower levels may be routinely detected in certain

tissues and cell types (e.g., lung, endothelial cells, liver, thymus, and other tissue of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
5 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of immune disorders and pulmonary and hepatic diseases. Its promoter may also be used for immune system and lung-
10 specific gene therapies. The expression of this gene in endothelial cells indicates that it may also involve in angiogenesis which therefore may play role in tumor matasis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

This gene is expressed primarily in liver, thyroid, parathyroid and to a lesser
15 extent in fetal lung, stomach and early embryos.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic regulation, obesity, hepatic failure, hepatocellular tumors or thyroiditis and thyroid tumors. Similarly,
20 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive/endocrine system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, thyroid, parathyroid, lung,
25 stomach, and embryonic tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and the extracellular locations indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of digestive/endocrine disorders, including metabolic regulation, hepatic failure, malabsorption, gastritis and neoplasms.

FEATURES OF PROTEIN ENCODED BY GENE NO: 43

This gene is expressed primarily in Schizophrenic adult brain, pituitary, front cortex, hypothalamus and to a lesser extent in retina, adipose and stomach cancer and placenta.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: schizophrenia and other neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nerve system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., retinal tissue, adipose, stomach, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in treatment/detection of disorders in the nerve
20 system, including schizophrenia, neurodegeneration, and neoplasia. Additionally, a secreted protein in brain may serve as an endocrine.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

 The translation product of this gene shares sequence homology with GTP
25 binding proteins which are thought to be important in signal transduction and protein transport.

 This gene is expressed primarily in umbilical vein and microvascular endothelial cells, GM-CSF treated macrophage, anergic T cells, osteoblast, osteoclast, CD34+ cells and to a lesser extent in gall bladder.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: bone formation and growth, osteonecrosis, osteoporosis, angiogenesis and/or hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and hematopoiesis systems, expression of this gene at significantly higher or lower levels

may be routinely detected in certain tissues and cell types (e.g., endothelial cells, blood cells, bone, and gall bladder, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene
5 expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to GTP binding proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment/detection of bone formation and growth, osteonecrosis, osteoporosis, and/or
10 hematopoiesis because its involvement in the growth signaling or angiogenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The translation product of this gene shares sequence homology with signal sequence receptor gamma subunit which is thought to be important in protein
15 translocation on endoplasmic reticulum.

This gene is expressed primarily in adrenal gland, salivary gland, prostate, and to a lesser extent in endothelial cells and smooth muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions: protein secretion. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the secretory organs, expression of this gene at significantly higher or lower levels may be
25 routinely detected in certain tissues and cell types (e.g., adrenal gland, salivary gland, prostate, endothelial cells, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
30 fluid from an individual not having the disorder.

The tissue distribution and homology to SSR gamma subunit indicate that polynucleotides and polypeptides corresponding to this gene are useful for endocrine disorders, prostate cancer, xerostomia or sialorrhea.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 46

This gene is expressed primarily in osteoclastoma cells and to a lesser extent in melanocyte, amygdala, brain, and stomach.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: ossification, osteoporosis, fracture, osteonecrosis, osteosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., melanocytes, amygdala, brain and other tissue of the nervous system, and stomach, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in intervention of ossification, osteoporosis, fracture, osteonecrosis and osteosarcoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

The translation product of this gene shares sequence homology with proline rich proteins which is thought to be important in protein-protein interaction.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological and psychological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nerve system and endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to proline-rich proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful in intervention

and detection of neurological diseases, including trauma, neoplasia, degenerative or metabolic conditions in the central nerve system. Additionally, the gene product may be a secreted by the brain as an endocrine.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 49

The translation product of this gene shares sequence homology with the AOCB gene from *Aspergillus nidulans* which is important in asexual development.

This gene is expressed primarily in infant brain and to a lesser extent in the developing embryo, trachea tumors, B-cell lymphoma and synovial sarcoma.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurodegenerative diseases, leukemia and sarcoma's. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
15 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, blood cells, trachea, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
20 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in infant brain and sarcoma's and homology to a gene involved in a key step of eukaryotic development (fungal spore formation) indicates
25 that the protein product of this clone could play a role in neurological diseases such as schizophrenia, particularly in infants. The existence of the gene in a B-cell lymphoma indicates the gene may be used in the treatment and detection of leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

30 This gene is expressed primarily in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: pulmonary disorders including lung cancer. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary system, expression of this gene at significantly higher or

lower levels may be routinely detected in certain tissues and cell types (e.g., lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene only in fetal lung indicates that it plays a key role in development of the pulmonary system. This would suggest that misregulation of the expression of this protein product in the adult could lead to lymphoma or sarcoma formation, particularly in the lung. It may also be involved in predisposition to certain pulmonary defects such as pulmonary edema and embolism, bronchitis and cystic fibrosis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 51

This gene is expressed primarily in hematopoietic cell types and fetal cells and to a lesser extent in all tissue types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in the immune system and hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene predominantly in hematopoietic cells and in the developing embryo indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and treatment of lymphomas and disease states affecting the immune system or hematopoiesis disorders such as leukemia, AIDS, arthritis and asthma..

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

This gene is expressed primarily in prostate and to a lesser extent in fetal spleen, fetal liver, infant brain and T cell leukemias.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: prostate disorders, prostate cancer, leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, and/or prostate gland expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., thymus, spleen, liver, brain and other tissue of the nervous system, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in prostate indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection or treatment of prostate disorders or prostate cancer. Its distribution in fetal liver and fetal spleen indicates it may play a role in the immune system and its misregulation could lead to immune disorders such as leukemia, arthritis and asthma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

The translation product of this gene shares sequence homology with dynein.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuro-degenerative diseases of the brain. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly neuro-degenerative diseases expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution in the brain and homology to dynein, a microtubule motor protein involved in the positioning of cellular organelles and molecules indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection/treatment of neurodegenerative diseases, such as Alzheimers, 5
Huntigtons, Parkinsons diseases and shizophrenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 54

The translation product of this gene shares sequence homology with ubiquitin-conjugation protein, an enzyme which is thought to be important in the processing of 10
the Huntingtons Disease causing gene.

This gene is expressed primarily in brain and to a lesser extent in activated macrophages.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a 15
biological sample and for diagnosis of diseases and conditions: neurodegenerative disease states including Huntington's disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of brain tissues. For a number of disorders of the above tissues or cells, particularly of the neurological systems expression of this gene at 20
significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level 25
in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution of this gene in the brain and its homology to a Huntington interacting protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the regulation of the expression of the Huntington disease gene and other neurodegenerative diseases including 30
spinocerebular ataxia types I and III, dentatorubropallidoluysian and spinal bulbar muscular atrophy. In addition, the existence of elevated levels of free ubiquitin pools in Alzheimer's disease, Parkinson's disease and amyotrophic lateral sclerosis indicates that the ubiquitin pathway of protein degradation plays a role in these disease states. Thus, considering the gene described here is homologous to a ubiquitin-conjugation 35
protein it may play a general role in neurodegenerative conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

This gene is expressed primarily in T-cells (anergic T-cells, resting T-Cells, apoptotic T-cells) and lymph node (breast), as well as brain (hypothalamus, hippocampus, pituitary, infant brain, early-stage brain).

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune (e.g. immunodeficiencies, autoimmunities, inflammation, leukemias & lymphomas) and neurological (e.g. Alzheimer's disease, dementia, schizophrenia) disorders. Similarly,
- 10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous, hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood
- 15 cells, lymphoid tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in the intervention or detection of pathologies associated with the hematopoietic and immune systems, such as anemias (leukemias). In addition, the expression in brain (including fetal) might suggest a role in developmental brain defects, neuro-degenerative diseases or behavioral abnormalities
- 25 (e.g. schizophrenia, Alzheimer's, dementia, depression, etc.).

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

- This gene is expressed primarily in lung, and to a lesser extent in a variety of other hematological cell types (e.g. Raji cells, bone marrow cell line, activated
- 30 monocytes).

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: pulmonary and/or hematological disfunction. Similarly, polypeptides and antibodies directed to these
- 35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculo-pulmonary and hematopoietic systems, expression of this

gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lung and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
5 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in the intervention and detection of pathologies associated with the vasculo-pulmonary system. In addition the expression of this gene
10 in a variety of leukocytic cell types and a bone marrow cell line might suggest a role in hematopoietic and immune system disorders, such as leukemias & lymphomas, inflammation, immunodeficiencies and autoimmunities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

15 The translation product of this gene shares sequence homology with adenylate kinase isozyme 3 (gil163528 GTP:AMP phosphotransferase (EC 2.7.4.10) [Bos taurus]), which is thought to be important in catalyzing the phosphorylation of AMP to ADP in the presence of ATP or inorganic triphosphate.

This gene is expressed primarily in fetal liver, heart and placenta, and to a lesser
20 extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatic, cardiovascular or reproductive disorders. Similarly, polypeptides and antibodies directed to these
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic, cardiovascular and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, heart, and placenta, and cancerous and wounded tissues) or
30 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
35 corresponding to this gene are useful for the treatment and diagnosis of conditions related to hepatic function and pathogenesis, in particular, those dealing with liver development and the differentiation of hepatocyte progenitor cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

This gene is expressed primarily in CD34 positive cells (Cord Blood).

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: hematopoietic
differentiation and immune disorders. Similarly, polypeptides and antibodies directed to
these polypeptides are useful in providing immunological probes for differential
identification of the tissue(s) or cell type(s). For a number of disorders of the above
10 tissues or cells, particularly of hematopoietic and immune systems, expression of this
gene at significantly higher or lower levels may be routinely detected in certain tissues
and cell types (e.g., hematopoietic cells, and blood cells, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
15 the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful in the detection and treatment of conditions
associated with CD34-positive cells, and therefore as a marker for cell differentiation in
20 hematopoiesis, as well as immunological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

The translation product of the predicted open reading frame of this contig has
sequence identity to the murine gene designated Insulin-Like Growth Factor-Binding
25 Protein (IGFBP)-1 as described by Lee and colleagues (Hepatology 19 (3), 656-665
(1994)).

This gene is expressed exclusively in hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
30 biological sample and for diagnosis of hemangiopericytoma and other pericyte or
endothelial cell proliferative disorders. Similarly, polypeptides and antibodies directed
to these polypeptides are useful in providing immunological probes for differential
identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of the circulatory and immune systems, expression of this
35 gene at significantly higher or lower levels may routinely be detected in certain tissues
and cell types (e.g., pericyte or endothelial cells, and liver, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Polynucleotides and polypeptides corresponding to this gene are useful as cell growth regulators since IGFBP-1-like molecules function as modulators of insulin-like growth factor activity. In addition, since IGFBP-1 is expressed at high levels following hepatectomy and during fetal liver development, polynucleotides of the present invention may also be used for the diagnosis of developmental disorders. Further, polypeptides of the present invention may be used therapeutically to treat developmental liver disorders as well as to regulate hepatocyte and supporting cell growth following hepatectomy or to treat liver disorders.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hemangiopericytoma and liver disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

This gene is expressed primarily in schizophrenic frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: nervous system and cognitive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the frontal cortex and CNS expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, treatment and diagnosis of frontal cortex, neuro-degenerative and CNS disorders

FEATURES OF PROTEIN ENCODED BY GENE NO: 62

This gene is expressed primarily in human adrenal gland tumor, and to a lesser extent in human kidney, medulla and adult pulmonary tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic, endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and nervous system disorders and neoplasia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adrenal gland, kidney, brain and other tissue of the nervous system, pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, treatment and diagnosis of neurological and endocrine disorders including neoplasia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

This gene is expressed primarily in human adipocytes, and to a lesser extent in spleen, 12-week old human, and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune, metabolic and growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipocytes, spleen, and testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of immune, developmental and metabolic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

One translated product of this clone is homologous to the mouse zinc finger protein PZF. (See Accession No. 453376; see also Gene 152 (2), 233-238 (1995).) Preferred polypeptide fragments correspond to the highly conserved domains shared between mouse and man. For example, preferred polypeptide fragments comprise the amino acid sequence: LQCEICGFTCRQKASLNWHMCKHDADSFYQFSCNICGKKFEKKDSVVAHKAKSH PEV (SEQ ID NO: 621); ITSTDILGTNPESLTQPSD (SEQ ID NO: 622); NSTSGECLLLEAEGM SKSY (SEQ ID NO: 623); CSGTERVSLMADGKIFVSGSSGGTEGLVMNSDILGATTEVLIEDSD SAGP (SEQ ID NO: 624); IQYVRCEMEGCGTVLAHPRYLQHIIKYQHLLKKKYVCPHPSCGRLF RLQKQLLRHAKHHT (SEQ ID NO: 625); DQRDYICEYCARAFKSSHNLAHVHRMIHTGEK (SEQ ID NO: 626); RSSRTSVSRHRDTENTRSSRSKTGSLQLICKSEPNTDQLDY (SEQ ID NO: 627); PFKDDPRDETYKPHLERETPKPRRKSG (SEQ ID NO: 630); QYVRCEMEGCGTVLAHPRYLQ HHIKYQHLLKKKYVCPHPSCGRLFRLQKQLLRHAKHHTD (SEQ ID NO: 629); or residues 151-182 of QRDYICEYCARAFKSSHNLAHVHRMIHTGEKHY (SEQ ID NO: 628). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in Rhabdomyosarcoma, melanocyte and colon cancer tissue and to a lesser extent in smooth muscle, pancreatic tumor, and apoptotic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hemopoetic, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., striated muscle, melanocytes, colon, smooth muscle, pancreas, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of cancer and hemopoetic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in human adipose and salivary gland tissue and to a lesser extent in human bone marrow and fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic and hemopoetic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipose, salivary gland, bone marrow, and kidney, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis of metabolic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This translated product of this gene was recently identified as oxytocinase splice variant 1. (See Accession Nos. 2209276 and d1010078.) Preferred polypeptide fragments comprise the amino acid sequence: EMFDSL SYFKGSSLLMLKTYLSEDVFQHAVVLYLHN HSYASIQSDDLWDSFNEVTNQTL DVKRMMKTWTLQKGFLVTVQKKGKELFIQGERFFLNMK PEIQPSDTRYM (SEQ ID NO: 631). Also preferred are polynucleotide fragments encoding this polypeptide fragment.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene is expressed primarily in hemopoetic cells, particularly apoptotic T-cells, and to lesser extent in primary dendritic cells and adipose tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of apoptotic T-cells, primary dendritic cells, and adipose tissue present in a biological sample and for diagnosis of diseases and conditions: hemopoetic diseases including cancer and general immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the oral and intestinal mucosa as well as hemopoetic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of diseases of the immune system, including cancer, hemopoetic and infectious diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

This gene is expressed primarily in kidney cortex and to a lesser extent in infant brain, heart, uterus, and blood.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of kidney tissue present in a biological sample and for diagnosis of diseases and conditions: soft tissue cancer, inflammation, kidney fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and endocrines systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, brain, and other nervous tissue, heart, uterus, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of cancer and fibroses.

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

The translation product of this gene shares strong sequence homology with vertebrate and invertebrate protein tyrosine phosphatases.

This gene is expressed primarily in endometrial tumors, melanocytes, myeloid progenitors and to a lesser extent in infant brain, adipocytes, and several hematopoietic stem cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of transformed hematopoietic and epithelial cells present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of skin and endometrium, leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, melanocytes, bone marrow, adipocytes, hematopoietic cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and sequence similarity with tyrosine phosphatases indicate that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of cancer and hematopoietic disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 70

This gene is expressed primarily in osteoclastoma, breast, and infant brain and to a lesser extent in various fetal and transformed bone, ovarian, and neuronal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: degenerative conditions of the brain and skeleton. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, mammary tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of degenerative, neurological and skeletal disorders.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 71**

This gene was originally cloned from tumor cell lines. Recently another group has also cloned this gene, calling it the human malignant melanoma metastasis-suppressor (KiSS-1) gene. (See Accession No. U43527.) Preferred polypeptide fragments comprise the amino acid sequence: LEKVASVGNSRPTGQQLSLGLLA (SEQ ID NO: 632); VHREEASCYCQAEPSTDL (SEQ ID NO: 633); RPALRQAGGGTREPRQKRWAGL (SEQ ID NO: 634); and AVNFRPQRSQSM (SEQ ID NO: 635). Any frame shifts can easily be resolved using known molecular biology techniques.

This gene is expressed primarily in many types of carcinomas and to a lesser extent in many normal organs.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissues(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly melanomas, and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
20 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of transformed organ tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
25 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. As a tumor suppressor gene, increase amounts of the polypeptide can be used to treat patients having a particular cancer.

30 The tissue distribution indicates that this gene and the translated product is useful for diagnosing and study of cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 72

This gene is expressed primarily in striatum and to a lesser extent in adipocytes and hemangiopericytoma.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of striatal cells present in a biological sample and for diagnosis of diseases and conditions: neurological, fat and lysosomal storage

diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., striatal tissue, adipocytes, and vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, study and treatment of neurodegenerative and growth disorders.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 73**

This gene is expressed primarily in bone marrow stromal cells and to a lesser extent in smooth muscle, testes, endothelium, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of bone marrow present in a biological sample and for diagnosis of diseases and conditions: connective tissue and hematopoietic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, stromal cells, smooth muscle, testes and other reproductive tissue, endothelium, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of connective tissue and blood diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

This gene is expressed primarily in brain, fetal liver and lung and to a lesser extent in retina, spinal chord, activated T-cells and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of brain and regenerating liver present in a biological sample and for diagnosis of diseases and conditions: CNS and spinal chord injuries, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
10 particularly of the nervous and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, pulmonary tissue, blood cells, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
15 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for study and treatment of hematopoietic and
20 neurological conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

The translation product of this gene shares sequence homology with GTP binding proteins (intracellular).

25 This gene is expressed primarily in bone marrow, brain, and melanocytes and to a lesser extent in various endocrine and hematopoietic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hematopoietic and
30 nervous system conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone
35 marrow, melanocytes, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to nucleotide binding factors indicate that polynucleotides and polypeptides corresponding to this gene are useful for study,
5 diagnosis, and treatment of brain degenerative, skin and blood diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

This gene is expressed primarily in activated T-cells and to a lesser extent in retina, brain, and fetal bone.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of activated T-cells and developing brain present in a biological sample and for diagnosis of diseases and conditions: immune deficiencies and skeletal and neuronal growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune, and skeletomuscular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, brain and other tissue of the nervous system, retinal tissue, and bone, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
25 corresponding to this gene are useful for diagnosis, study and treatment of cancer, urogenital, and brain degenerative diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This gene is expressed primarily in fetal liver, activated monocytes, osteoblasts
30 and to a lesser extent in synovial, brain, and lymphoid tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of myeloid and lymphoid present in a biological sample and for diagnosis of diseases and conditions: inflammation, immune deficiencies, cancer. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and skeleton, expression of this gene at significantly

higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, blood cells, bone, synovial tissue, brain and other tissue of the nervous system, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
5 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of lymphoid
10 and mesenchymal cancers and nervous system diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 78

The translation product of this gene shares sequence homology with polymerase polyprotein precursor which is thought to be important in DNA repair and replication
15 This gene is expressed primarily in infant brain and to a lesser extent in tumors and tumor cell lines

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
20 not limited to, especially of the neural system and developing organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system expression of this gene at significantly higher or lower levels may be routinely detected
25 in certain (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to polymerase polyprotein precursor indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers especially of the neural system and developing
30 organs

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 79

This gene is expressed primarily in muscle and endothelial cells and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: vascular diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., muscle, endothelial cells, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders of the vascular and neural system including cardiovascular and endothelial.

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

This gene is expressed primarily in placenta and to a lesser extent in fetal liver. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: developmental disorders and disorder of the haemopoietic system, fetal liver and placenta. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developmental disorders and disorder of the haemopoietic system, fetal liver and placenta, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of developmental disorders and disorders of the haemopoietic system, fetal liver and placenta.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

This gene is expressed primarily in bone marrow, placenta and tissues and organs of the hematopoietic system.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorders of the bone and haemopoietic system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, bone and hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, placenta, and hematopoietic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the
20 immune, bone and hematopoietic system

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

The translation product of this gene shares sequence homology with secretory carrier membrane protein which is thought to be important in protein transport and
25 export. Any frame shifts in coding sequence can be easily resolved using standard molecular biology techniques. Another group recently cloned this gene, calling it SCAMP. (See Accession No. 2232243.)

This gene is expressed primarily in prostate, breast and spleen, and to a lesser extent in several other tissues and organs.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorders of the breast prostate and spleen. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
35 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly disorders of the breast prostate and spleen, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell

types (e.g., prostate, mammary tissue, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to secretory carrier membrane protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the breast, prostate and spleen.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 83**

This gene is expressed primarily in developing organs and tissue like placenta and infant brain and to a lesser extent in developed organs and tissue like cerebellum and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, heart, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases of the neural system including neurological disorders and cancer.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 84

The translation product of this gene shares sequence homology with ATPase 6 in *Trypanosoma brucei* which is thought to be important in metabolism.

This gene is expressed primarily in tumor and fetal tissues and to a lesser extent in melanocytes, kidney cortex, monocytes and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions: metabolism disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissues, melanocytes, kidney, blood cells, ovary and other tissue of the reproductive system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ATPase indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of metabolism disorders, especially in fetal and tumor tissue growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

The translation product of this gene shares sequence homology with the immunoglobulin superfamily of proteins which are known to be important in immune response and immunity.

This gene is expressed primarily in stromal cells, colon cancer, lung, amygdala, melanocyte and to a lesser extent in a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of stromal cell development and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the stromal cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., stromal cells, colon, lung, amygdala, and melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to immunoglobulin indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of immune system disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

The translation product of this gene shares sequence homology with transcription initiation factor eIF-4 gamma which is thought to be important in gene transcription.

This gene is expressed primarily in tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumorigenesis.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly in tumor tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to transcription initiation factor eIF-4 gamma indicate that polynucleotides and polypeptides corresponding to this gene are useful for gene regulation in tumorigenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 87

The translation product of this gene shares sequence homology at low level in prolines with secreted basic proline-rich peptide II-2 which is thought to be important in protein structure or inhibiting hydroxyapatite formation in vitro.

This gene is expressed primarily in endometrial tumor and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: endometrial tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular/skeletal and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample

taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to secreted basic proline-rich peptide II-2
5 indicate that polynucleotides and polypeptides corresponding to this gene are useful for inhibiting hydroxyapatite formation or establishing cell/tissue structure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 88

This gene is expressed primarily in: amniotic cells induced with TNF in culture;
10 and to a lesser extent in colon tissue from a patient with Crohn's Disease; parathyroid tumor; activated T-cells; cells of the human Caco-2 cell line; adenocarcinoma; colon; corpus colosum; fetal kidney; pancreas tumor; fetal brain; early stage brain, and anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system;
20 e.g., tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., amniotic cells, colon, kidney, pancreas, parathyroid, brain and other tissue of the nervous system, blood cells, hematopoietic cells, liver, spleen, bone, testes and other reproductive tissue, brain and other tissue of the nervous system, and epithelial cells, and cancerous and wounded tissues) or bodily fluids (e.g.,
25 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful
30 for modulating tumorigenesis and other immune system conditions such as disorders in immune response.

FEATURES OF PROTEIN ENCODED BY GENE NO: 89

This gene is expressed primarily in fetal liver/spleen and hematopoietic cells and
35 to a lesser extent in brain, osteosarcoma, and testis tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions: leukemia and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, liver, spleen, bone, testes, and other reproductive tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hematopoietic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 90

The translation product of this gene shares weak sequence homology with mouse Gcap1 protein which is developmentally regulated in brain.

This gene is expressed primarily in infant and adult brain and fetal liver/spleen and to a lesser extent in smooth muscle, T cells, and a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, hematopoietic, immune, and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, blood cells, liver, spleen, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and its homology to Gcap1 protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders in neuronal, hematopoietic, immune, and endocrine systems.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 91

This gene is expressed primarily in brain and hematopoietic cells and to a lesser extent in tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorder in nervous, hematopoietic, immune systems and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, hematopoietic, immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of disorders in the nervous, hematopoietic, and immune systems.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 92

The translation product of this gene shares sequence homology with neuroendocrine-specific protein A which is thought to be important in neurologic systems.

30

This gene is expressed primarily in brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neural disorders and degeneration disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central or peripheral nervous systems, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to neuroendocrine-specific protein A indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of neural disorders and degeneration disease.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 93

The translation product of this gene shares sequence homology with collagen-like protein and prolin-rich protein which are thought to be important in connective tissue function and tissue structure.

15 This gene is expressed primarily in fetal liver/spleen and brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuronal or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these
20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and brain and other tissue of the nervous system, and
25 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to collagen-like protein and proline-rich
30 proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for supporting brain and hematopoietic tissue function and diagnosis and treatment of disorders in these functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 94

35 This gene is expressed primarily in embryonic tissues and tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system (e.g., tumors), expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancer.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 95**

This gene is expressed primarily in brain tumor, placenta, and melanoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain tumor or melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain or melanocytes, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, placenta, and melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the translation product of this gene is useful in the diagnosis and treatment of brain tumors and melanoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 96

The translation product of this gene shares sequence homology with a yeast membrane protein, SUR4, which encodes for APA1 that acts on a glucose-signaling pathway that controls the expression of several genes that are transcriptionally regulated by glucose.

This gene is expressed primarily in fetal liver, and to a lesser extent in placenta and breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of fetal liver or defects of glucose-regulated ATPase activities in tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal immune/hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, placenta, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to yeast SUR4 membrane protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of defects of fetal liver or defects of glucose-regulated ATPase activities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 97

This gene is expressed primarily in fetal liver, brain, and amniotic fluid.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the fetal immune system and adult brain. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal immune system and adult brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., amniotic fluid, serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for detecting defects of the fetal immune and hematopoietic systems since fetal liver is

the predominant organ responsible for hematopoiesis in the fetus. In addition, the gene product of this gene is thought to be useful for detecting certain neurological defects of the brain.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 98**

The translation product of this gene shares sequence homology with an yolk protein precursor, Vitellogenin which is thought to be important in binding lipids such as phosvitin.

This gene is expressed primarily in amniotic cells and fetal liver.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in amniotic cells, fetal liver development and the fetal immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., amniotic cells, and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
20 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution and homology to vitellogenin indicate that the protein product of this clone is useful for treatment and diagnosis of defects in amniotic cells, fetal liver development and the fetal immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 99

30 This gene is expressed primarily in placenta, endometrial tumor, osteosarcoma and stromal cells.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumor of the endometrium or bone, and osteosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the obstetric system (e.g. placenta,

endometrium) and the bones, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, endometrium, bone, and stromal cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumors and abnormalities of the endometrium, and the bones because of its abundance in the aforementioned tissues..

FEATURES OF PROTEIN ENCODED BY GENE NO: 100

This gene is expressed primarily in hepatocellular tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatocellular tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of hepatocellular cancer because of its abundant expression in this tissue.

FEATURES OF PROTEIN ENCODED BY GENE NO: 101

This gene is expressed primarily in Corpus Colosum, fetal lung and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the Corpus Colosum or defects of the fetal lung. Similarly, polypeptides and antibodies directed to

these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Corpus Colosum and brain in general, and fetal lung, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lung, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of defects of the Corpus Colosum and brain in general, and defects of fetal lung.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 102**

This gene is expressed primarily in T cells and stromal cells, and to a lesser extent in adrenal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of T cell immunity and stromal cell development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, stromal cells, and adrenal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of defects of T cell immunity and stromal cell development because of its abundant expression in these tissues.

35 **FEATURES OF PROTEIN ENCODED BY GENE NO: 103**

This gene is expressed primarily in infant brain and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the brain and nervous system. Similarly, polypeptides and antibodies directed to these polypeptides
5 are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, especially brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and placenta, cancerous and
10 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful
15 for detecting defects of the brain, especially in young children.

FEATURES OF PROTEIN ENCODED BY GENE NO: 105

This gene is expressed primarily in human osteoclastoma and to a lesser extent in human pancreas tumor.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly osteoclastoma and pancreatic tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
25 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly in transformed tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone and pancreas, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of some types of tumors, particularly pancreatic cancer and
35 osteoclastoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 106

This gene is expressed primarily in fetal liver/spleen, and to a lesser extent in activated T-Cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of immune disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 107

This gene is expressed primarily in human embryo and to a lesser extent in spleen and chronic lymphocytic leukemia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for the diagnosis and treatment of leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 108

This gene is expressed primarily in placenta, and to a lesser extent in early stage human brain and in lung.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: fetal developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
10 or cell type(s). For a number of disorders of the above tissues or cells, particularly in fetal and amniotic tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, brain and other tissue of the nervous system, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
15 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this is useful for production of growth factor(s) associated with fetal development. Preferred
20 polypeptides comprise the full-length polypeptide shown in the sequence listing, truncated however, at the amino terminus and beginning with QTIE.

FEATURES OF PROTEIN ENCODED BY GENE NO: 109

This gene is expressed primarily in fetal spleen, and to a lesser extent in B-Cell
25 lymphoma and T-Cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
30 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., spleen and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
35 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for the treatment and diagnosis of human lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 110

5 The translation product of this gene shares sequence homology with sarcoma amplified sequence (SAS), a tetraspan receptor which is thought to be important in malignant fibrous histiocytoma and liposarcoma.

 This gene is expressed primarily in human osteoclastoma, and to a lesser extent in pineal gland and infant brain.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: malignant fibrous histiocytoma and liposarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, pineal gland, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to sarcoma amplified sequence (SAS) indicate that the protein product of this clone is useful for treatment of, osteosarcoma,
25 malignant fibrous histiocytoma and liposarcoma and related cancers, particularly sarcomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 111

 The translation product of this gene shares sequence homology with 6.8K
30 proteolipid protein, mitochondrial - bovine.

 This gene is expressed primarily in Wilm's tumor and to a lesser extent in cerebellum and placenta.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: Wilm's tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the immune or renal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to 6.8K proteolipid protein indicate that the protein product of this clone is useful for diagnostic and therapeutics associated with tumors, particularly Wilm's tumor disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 112

This gene is expressed primarily in embryonic tissue and to a lesser extent in osteoblasts, endothelial cells, macrophages (GM-CSF treated), and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, bone, endothelial cells, blood cells and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of immune disorders. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: MITDVQLAIFANMLGVSLFLLVVLYHYVAVNNPKKQE (SEQ ID NO: 636).

FEATURES OF PROTEIN ENCODED BY GENE NO: 113

This gene is expressed primarily in hepatocellular tumor, and to a lesser extent in fetal liver/spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors, particularly hepatocellular tumors. Similarly, polypeptides and antibodies directed to these

5 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

10 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful

15 for diagnosis and treatment of tumors, particularly hepatocellular tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 114

The translation product of this gene exhibits a very high degree of sequence identity with the human Pig8 gene which is thought to be important in p53 mediated

20 apoptosis. The sequence of this gene has since been published by Polyak and colleagues (Nature 389, 300-306 (1997)). In addition, the predicted translation product of this contig exhibits very high sequence homology with a murine gene denoted as EI24 which is also thought to be important in p53 mediated apoptosis.

This gene is expressed primarily in infant brain and activated T-cells and to a

25 lesser extent in bone marrow, fetal liver, and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and tissue damage by radiation and anti-cancer drugs. Similarly,

30 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the

35 nervous system, blood cells, bone marrow, liver, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to human Pig8 and murine EI24 genes indicate that polynucleotides and polypeptides corresponding to this gene are useful for preventing apoptosis in patients being treated with anti-oncogenic drugs such as etoposide, hydroperoxycyclophosphamide, and X-irradiation, since this protein product is upregulated in cells undergoing such treatment where p53 was overexpressed. It may also be useful in the treatment of hematopoietic disorders and in boosting numbers of hematopoietic stem cells by interfering with the apoptosis of progenitor cells. The mature polypeptide is predicted to comprise the following amino acid sequence:

5 EEMADSVKTFLLQDLARGIKDSIWGICTISKLDARIQQKREEQRRRRASSVLAQRRRAQSIERKQES
 10 EPRIVSRIFQCCAWNGGVFWFSLLLFYRVFIPVLQSVTARIIGDPSLHGDVWSWLEFFLTSIFSA
 LWVLPLFVLSKVVNIAWFQDIADLAFEVSGRKPHFPSPVSKIIADMLFNLLLQALFLIQGMFVSL
 FPIHLVGQLVSLHMSLLYSLYCFEYRWFNKGIEMHQRLSNIERNWPYYFGFGLPLAFLTAMQ
 15 SSYIISGCLFSILFPLFIISANEAKTPGKAYLFQLRLFSLVVFLSNRLFHKTVYLQSALSSSTSAAEK
 FPSPHPSPAKLKATAGH (SEQ ID NO: 637). Accordingly, polypeptides comprising the foregoing amino acid sequence are provided as are polynucleotides encoded such polypeptides.

20 **FEATURES OF PROTEIN ENCODED BY GENE NO: 115**

This gene is expressed primarily in stromal cells and to a lesser extent in multiple sclerosis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: affecting the nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., stromal cells and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of multiple sclerosis and other autoimmune diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 116

This gene is expressed primarily in the gall bladder

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: gall stones or infection
of the digestive system. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
10 particularly of the digestive system or renal system, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., gall bladder and tissue of the digestive system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
15 the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for possible prevention of digestive disorders
where there may be a lack of digestive enzymes produced or in the detection and
20 possible prevention of gall stones.

FEATURES OF PROTEIN ENCODED BY GENE NO: 117

The translation product of this gene shares sequence homology with dystrophin
gene which is thought to be important in building and maintenance of muscles.

25 This gene is expressed primarily in placenta and to a lesser extent in fetal brain
and fetal liver, and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: muscular dystrophy,
30 Duchenne and Becker's muscular dystrophies. Similarly, polypeptides and antibodies
directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the skeletal muscle system, expression of this
gene at significantly higher or lower levels may be routinely detected in certain tissues
35 and cell types (e.g., placenta, brain and other tissue of the nervous system, muscle,
liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from

an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to the dystrophin gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diseases related the degenerative myopathies that are characterized by the weakness and atrophy of muscles without neural degradation; such as Duchenne and Becker's muscular dystrophies.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 118**

This gene is expressed primarily in olfactory tissue and to a lesser extent in cartilage.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions: connective tissue diseases; chondrosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the connective tissue, expression of this gene at significantly higher or
20 lower levels may be routinely detected in certain tissues and cell types (e.g., olfactory tissue and cartilage, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
25 disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for tumors of connective tissues, osteoarthritis and the treatment and diagnosis of chondrosarcoma.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 119**

This gene is expressed primarily in Activated Neutrophils and to a lesser extent in fetal spleen, and CD34 positive cells from cord blood.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: allergies, defects in hematopoiesis and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential

identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and hematopoiesis system the, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and spleen, and cancerous and
5 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for reducing the allergic effects felt by allergy suffers by neutralizing the activity of the immune system, especially since neutrophils are abundant in persons suffering from allergies and other inflammatory conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 120

15 The translation product of this gene shares sequence homology with poly A binding protein II which is thought to be important in RNA binding for transcription of RNA to DNA

This gene is expressed primarily in colon and to a lesser extent in brain and immune system.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: colon cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
25 number of disorders of the above tissues or cells, particularly of the immune and digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., colon, tissue and cells of the immune system, and brain or other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
30 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to poly A binding protein II indicate that polynucleotides and polypeptides corresponding to this gene are useful for detection
35 and treatment of colon cancer and other disorders of the digestive system..

FEATURES OF PROTEIN ENCODED BY GENE NO: 121

The translation product of this gene shares sequence homology with thymidine diphosphoglucose 4.6 dehydrase which is thought to be important in the metabolism of sugar.

- 5 This gene is expressed primarily in fetal liver and spleen and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diabetes. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 15 20 The tissue distribution and homology to thymidine diphosphoglucose 4.6 dehydrase indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of persons with diabetes since it appears that this protein is needed in the metabolism of sugar in to its more basic components.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 122**

The translation product of this gene shares sequence homology with ceruloplasmin which is thought to be important in the metabolism and transport of iron and copper. Ceruloplasmin also contains domains with homology to clotting factors V and VIII. Defects in the circulating levels of ceruloplasmin (aceruloplasminemia) have been associated with certain disease conditions such as Wilson disease, and the accompanying hepatolenticular degeneration.

This gene is expressed primarily in brain and retina and to a lesser extent in endothelial cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases marked by defects in iron metabolism; aceruloplasminemia not characterized by defects in the
- 35

known ceruloplasmin gene locus; nonclassical Wilson disease; movement disorders; and tumors derived from a brain tissue origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, retina, and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, retinal tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ceruloplasmin indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of patients with aceruloplasminemia, or other defects in iron and/or copper metabolism. Mutations in this locus could also be diagnostic for patients currently experiencing or predicted to experience aceruloplasminemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 123

This gene is expressed primarily in brain and B cell lymphoma and to a lesser extent in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: B cell lymphoma; tumors and diseases of the brain and/or spleen; hematopoietic defects. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, blood cells, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders in neuronal,

hematopoietic, and immune systems. It could potentially be useful for neurodegenerative disorders and neuronal and/or hematopoietic cell survival or proliferation.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 124**

This gene is expressed primarily in osteoclastoma, dermatofibrosarcoma, and B cell lymphoma and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer in particular osteoclastoma, dermatofibrosarcoma, and B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, immune, and circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, epidermis, blood cells, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers and lymphoma; osteoporosis; and the control of cell proliferation and/or differentiation.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 125

This gene is expressed primarily in immune tissues and hematopoietic cells, particularly in activated T cells and neutrophils, spleen, and fetal liver, and to a lesser extent in infant adrenal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in T cell activation; hematopoietic disorders; tumors of a hematopoietic and/or adrenal gland origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and/or endocrine systems, expression of this gene at significantly higher

or lower levels may be routinely detected in certain tissues and cell types (e.g., cells and tissues of the immune system, hematopoietic cells, blood cells, liver, and adrenal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
5 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune and/or hematopoietic disorders;
10 diseases related to proliferation and/or differentiation of hematopoietic cells; defects in T cell and neutrophil activation and responsiveness; and endocrine and/or metabolic disorders, particularly of early childhood.

FEATURES OF PROTEIN ENCODED BY GENE NO: 126

15 This gene is expressed primarily in placenta and endothelial cells and to a lesser extent in melanocytes and embryonic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of an endothelial
20 cell origin; angiogenesis associated with tumor development and metastasis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system and developing embryo, expression of this gene at significantly higher or lower levels
25 may be routinely detected in certain tissues and cell types (e.g., placenta, endothelial cells, melanocytes, and embryonic tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
30 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of developmental disorders; inhibition of angiogenesis; and vascular patterning.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 127

This gene is expressed primarily in endothelial cells and hematopoietic tissues, including spleen, tonsils, leukocytes, and both B- and T-cell lymphomas.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of an endothelial cell and/or hematopoietic origin; leukemias and lymphomas. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, hematopoietic cells, spleen, tonsils, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the manipulation of angiogenesis; the differentiation and morphogenesis of endothelial cells; the proliferation and/or differentiation of hematopoietic cells; and the commitment of hematopoietic cells to distinct cell lineages.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 128

This gene is expressed primarily in kidney medulla and to a lesser extent in spleen from chronic myelogenous leukemia patients, prostate cancer, and some other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of a kidney origin; chronic myelogenous leukemia; prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney and spleen, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, spleen, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of kidney disorders and cancer, particularly chronic myelogenous leukemia and prostate cancer. It may also be useful for the enhancement of kidney tubule regeneration in the treatment of acute renal failure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 129

This gene is expressed primarily in adult and infant brain and to a lesser extent in mesenchymal or fibroblast cells, as well as tissues with a mesenchymal origin.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of a brain and/or mesenchymal origin; neurodegenerative disorders; cancer; fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and of mesenchymal cells and tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of tumors of a brain and/or mesenchymal origin; neurodegenerative disorders; cancer; and fibrosis, based upon the expression of this gene within those tissues. Fibrosis is considered as mesenchymal cells and fibroblasts are the primary cellular targets involved in this pathological condition.

FEATURES OF PROTEIN ENCODED BY GENE NO: 130

This gene is expressed primarily in hepatocellular cancer and to a lesser extent in fetal tissues as well as testes tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: liver cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, fetal tissue, and testes and other
5 reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of liver cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 131

This gene is expressed only in infant early brain.

- 15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: development and diseases of the nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
20 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
25 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the brain in children and in
30 treating nervous system disorders such as Alzheimer's disease, schizophrenia, dementia, depression, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 132

This gene is expressed primarily in brain and to a lesser extent in glioblastoma.

- 35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Alzheimer's disease,

schizophrenia, depression, mania, and dementia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating brain disorders such as Alzheimer's disease, schizophrenia, depression, mania, and dementia.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 133**

The translation product of this gene shares sequence homology with ribitol dehydrogenase of bacteria which is thought to be important in metabolism of sugars.

This gene is expressed primarily in macrophage and to a lesser extent in T-cell lymphoma and lung.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tissue destruction in inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and homology to ribitol dehydrogenase indicate that polynucleotides and polypeptides corresponding to this gene are useful for altering macrophage metabolism in diseases such as inflammation where macrophages are causing excess tissue destruction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 134

This gene is expressed primarily in pancreatic tumor and to a lesser extent in synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions which include, but are
not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are
useful in providing immunological probes for differential identification of the tissue(s)
or cell type(s). For a number of disorders of the above tissues or cells, particularly of
10 the endocrine and connective tissue systems, expression of this gene at significantly
higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,
pancreas, and synovial tissue, and cancerous and wounded tissues) or bodily fluids
(e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
sample taken from an individual having such a disorder, relative to the standard gene
15 expression level, i.e., the expression level in healthy tissue or bodily fluid from an
individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for treating and diagnosing various cancers.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 135

This gene is expressed primarily in T cell lines such as Raji and to a lesser
extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions: immune system
disorders and inflammation. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the immune system, expression of this gene at significantly higher or
30 lower levels may be routinely detected in certain tissues and cell types (e.g., blood
cells, and brain and other tissue of the nervous system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
35 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for treating and diagnosing inflammatory diseases

such as rheumatoid arthritis, sepsis, inflammatory bowel disease, and psoriasis, as well as neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 136

5 The translation product of this gene shares high sequence homology with SAR1 subfamily of GTP-binding proteins which is thought to be important in vesicular transport in mammalian cells.

 This gene is expressed primarily in serum-stimulated smooth muscle cells and to a lesser extent in a T-cell lymphoma.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases affecting vesicular transport. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
20 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to GTP-binding proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for gene therapy
25 in treating the large number of diseases involved in defective vesicular transport within cells..

FEATURES OF PROTEIN ENCODED BY GENE NO: 137

 The translation product of this gene shares sequence homology with a protein
30 found in *C. elegans* cosmid F25B5.

 This gene is expressed primarily in a fetal tissues and to a lesser extent in melanocytes.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: abnormal fetal development, especially of the pulmonary system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal pulmonary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, pulmonary tissue, and melanocytes, and
5 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for treatment and diagnosis of diseases affecting the pulmonary system, such as emphysema.

FEATURES OF PROTEIN ENCODED BY GENE NO: 138

This gene is expressed primarily in gall bladder and to a lesser extent in smooth
15 muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: digestive system disease and gall bladder problems. Similarly, polypeptides and antibodies directed to these
20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., gall bladder and tissue of the digestive system, and smooth muscle, and cancerous and
25 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for treating diseases of the digestive system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 139

This gene is expressed primarily in placenta and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: abnormal fetal development. Similarly, polypeptides and antibodies directed to these polypeptides are

useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developing tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, and brain and other
5 tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing abnormal fetal development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 140

15 This gene is expressed primarily in smooth muscle and to a lesser extent in ovary, prostate cancer, and activated monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hypertension and
20 atherosclerosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., smooth
25 muscle, ovary and other reproductive tissue, prostate, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the circulatory system, such as hypertension, atherosclerosis, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 141

35 This gene is expressed primarily in fetal spleen and to a lesser extent in placenta and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: anemia and other diseases affecting blood cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., spleen, placenta, bone marrow, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the generation of red and white blood cells and for the diagnosis of disease of these cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 142

The predicted translation product of this contig is a human homolog of the murine tetracycline/sugar transporter molecule recently reported by Matsuo and colleagues (Biochem. Biophys. Res. Commun. 238 (1), 126-129 (1997)).

This gene is expressed primarily in synovium and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: rheumatoid arthritis and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and lymphatic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory diseases, such as rheumatoid arthritis, leukemia, neutropenia, inflammatory bowel disease, psoriasis, sepsis, and the like.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 143

This gene is expressed primarily in placenta and to a lesser extent in melanocyte, fetal liver and spleen, and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: abnormal early development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, lower levels
15 may be routinely detected in certain tissues and cell types (e.g., placenta, melanocytes, liver, spleen, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
20 individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of abnormal early development phenomena and diseases.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 144

This gene is expressed primarily in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: anemia and neutropenia.
30 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and blood systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver and spleen,
35 and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the

expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in hematopoiesis and bone marrow regeneration as it is most abundant in fetal tissues responsible for the generation of hematopoietic cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 145

The translation product of this gene shares sequence homology with protein tyrosine phosphatase which is thought to be important in transducing signal to activate cells such as T cell, B cell and other cell types.

This gene is expressed primarily in T cells and tissues in early stages of development and to a lesser extent in cancers.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-related diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic and fetal tissue, undifferentiated cells, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the protein tyrosine phosphatase family indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 146

This gene is expressed primarily in T cell and to a lesser extent in B cell, macrophages and tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating the immune system therefore can be used in treating diseases such as autoimmune diseases and cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 147

This gene is expressed primarily in placenta and to a lesser extent in endothelial cells, testis tumor, ovarian cancer, uterine cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, endothelial cells, testis and ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 148

This sequence has significant homology to mouse torsin A. Recently, another group cloned the human Torsin A gene. (See, Accession No. 2358279; see also Nature Genet. 17, 40-48 (1997).)

This gene is expressed primarily in osteoclastoma, T-cell, and placenta and to a lesser extent in fetal lung, fetal liver, fetal brain, adult brain and tumor tissues

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disease conditions in hematopoiesis and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoiesis system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, bone, placenta, lung, liver, and brain and other tissues of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating blood related diseases such as deficiencies in red blood cell, white blood cell, platelet and other hematopoiesis cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 149

This gene is expressed primarily in T cell, prostate and prostate cancer, endothelial cells and to a lesser extent in monocyte, dendritic cell, bone marrow, salivary gland, colon cancer, stomach cancer, pancreatic tumor, uterine cancer, fetal spleen and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-related diseases and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, prostate, endothelial cells, dendritic cells, bone marrow, salivary gland, colon, stomach, pancreas, uterus, spleen and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 150

- 5 This gene was recently cloned by another group, calling it eIF3-p66. (See Accession No. 2351378.) This gene plays a role in RNA binding and macromolecular assembly, and therefore, any mutations in this gene would likely result in a diseased phenotype. Preferred polypeptide fragments comprise the amino acid sequence:
- MAKFMTPVIQDNPSGWGPCAVPEQFRDMPYQPFSGDRLGKVADWTGATYQDKRYTNKYSS
- 10 QFGGGSQYAYFHEEDESSFLVDTARTQKTAYQRNRMFAQRNLRRDKDRRNMLQFNQLP
KSAKQKERERIRLQKKFQKQFGVRQKWDQKSQKPRDSSVEVRSDWEVKEEMDFPQLMKMRY
LEVSEPQDIECCGALEYDKAFDRIITRSEKPLRXXXKRIFHTVTTDDPVIRKLAKTQGNVFATD
AILATLMSCTRSVYSWDIVVQRVGSKLFFDKRDNSDFLLTVSETANEPPQDEGNSFNSPRNL
AMEATYINHNFSQQCLRMGKERYNFPNPNPFVEDDMDKNEIASVAYRYSGLGDDIDLIVRC
- 15 EHDGVMGTANGEVSFINIKTLNEWDSRHCNGVDWRQKLD SQRGAVIATELKNNSYKLARWTC
CALLAGSEYLKLGYSRYHVKDSSRHVILGTQQFKPNEFASQINLSVENAWGILRCVIDICMKL
EEGKYLLKDPNKQVIRVYSLPDGTFSS (SEQ ID NO: 638), as well as N-terminal and C-terminal deletions of this polypeptide fragment.

- 20 This gene is expressed primarily in T cell, bone marrow, embryo and endothelial cells and to a lesser extent in testis tumor and endometrial tumor.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune diseases and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful
- 25 in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
- 30 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune disorders and cancers.
- 35

FEATURES OF PROTEIN ENCODED BY GENE NO: 151

This gene is expressed primarily in testis and to a lesser extent in T cell, spinal cord, placenta, neutrophil and monocyte.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: male reproductive and endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive, immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testis and other reproductive tissue, blood cells, tissue of the nervous system, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating immune and reproductive functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 152

The translation product of this gene shares sequence homology with tyrosyl-tRNA synthetase which is thought to be important in cell growth.

This gene is expressed primarily in brain, liver, keratinocytes, tonsils, and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, keratinocytes, tonsils, heart expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissues of the nervous system, liver, keratinocytes, tonsils and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard

gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to tyrosyl-tRNA synthetase indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating cell growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 153

This gene is homologous to the *Drosophila* transcriptional regulator dre4. (See Accession No. 2511745.) Dre4 is a gene required for steroidogenesis in *Drosophila melanogaster* and encodes a developmentally expressed homologue of the yeast transcriptional regulator CDC68. Preferred polypeptide fragments comprise the amino acid sequence: KKRHTDVQFYTEVGEITTDLGKHQHMHDRDDLYAEQMEREMRHKLKTAFFKNFIEKVEALTKEELEFEVPPFDLGFNGAPYRSTCLLQPTSSALVNATEWPPFVVTLDEVELIHFXRVQFHLKNFDMVIVYKDYSKKVTMINAIPVASLDPIKEWLNSCDLKYTEGVQSLNWTIMKTTVDPEGFFEQGGWSFL (SEQ ID NO: 639), as well as N-terminal and C-terminal deletions of this fragments. Also preferred are polynucleotide fragments encoding this polypeptide fragment.

This gene is expressed primarily in fetal liver, spleen, placenta, lung, T cell, thyroid, testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain tumor, heart and liver diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal liver, spleen, placenta, lung, T cell, thyroid, testes expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, placenta, lung, blood cells, thyroid, and testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 154

This gene is expressed primarily in brain and to a lesser extent in fetal heart, testis, spleen, lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: heart, liver and spleen diseases, immunological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, fetal heart, testis, spleen, lung expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, heart, testes and other reproductive tissue, spleen, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 155

Activation of T cells through the T cell antigen receptor (TCR) results in the rapid tyrosine phosphorylation of a number of cellular proteins, one of the earliest being a 100 kDa protein. This gene is the human equivalent of murine valosin containing protein (VCP). VCP is a member of a family of ATP binding, homo-oligomeric proteins, and the mammalian homolog of *Saccharomyces cerevisiae* cdc48p, a protein essential to the completion of mitosis in yeast. Both endogenous and expressed murine VCP are tyrosine phosphorylated in response to T cell activation. Thus we have identified a novel component of the TCR mediated tyrosine kinase activation pathway that may provide a link between TCR activation and cell cycle control.

25

This gene is expressed primarily in brain, liver, spleen, placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, spleen, placenta expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, spleen, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from

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an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to VCR indicate that polynucleotides and polypeptides corresponding to this gene are useful for treating cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 156

The translation product of this gene shares sequence homology with rat growth response protein which is thought to be important in cell growth. A group recently
10 cloned the human homolog of this gene, calling it insulin induced protein 1. (See Accession No. 2358269, see also, Genomics 43 (3), 278-284 (1997).) Preferred polypeptide fragments comprise the amino acid sequence: RSGGLGTTIAFLATLITQF LVYNGVYQYTSPDFLYIRSWLPCIFFSGGVTGNIGRQLAMGVPEKPHSD (SEQ ID NO: 640), as well as N-terminal and C-terminal deletions of this polypeptide fragment. Also
15 preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in brain, liver, placenta, heart, spleen, lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, placenta, heart, spleen.
25 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, placenta, heart, spleen, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
30 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to growth-response protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating cell growth.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 157

This gene is expressed primarily in Glioblastoma, endometrial tumor, lymphoma and pancreas tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Glioblastoma, Endometrial tumor, lymphoma and pancreas tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, lymphoid tissue, pancreas, and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 158

The translation product of this gene shares sequence homology with IGE receptor which is thought to be important in allergy and asthma.

This gene is expressed primarily in T cell, and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: allergy and asthma and other immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to IgE receptor indicate that polynucleotides and polypeptides corresponding to this gene are useful for allergy and asthma.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 159**

The translation product of this gene shares sequence homology with immunoglobulin heavy chain which is thought to be important in immune response to the antigen.

10 This gene is expressed primarily in activated neutrophil and to a lesser extent in activated T cell, monocyte and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: infection, inflammation and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are
15 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
20 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to immunoglobulin heavy chain variable region indicate that polynucleotides and polypeptides corresponding to this gene are
25 useful for making the ligand to block specific antigen which cause certain disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 160

The translation product of this gene shares sequence homology with mouse X inactive specific transcript protein which is thought to be important in X chromosome
30 inactivation.

This gene is expressed primarily in HSA172 cell and to a lesser extent in normal ovary tissue, ovarian cancer, frontal cortex and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: ovarian tumor, schizophrenia and other neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovary and other reproductive tissue, and brain and other
5 tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution and homology to X inactive specific transcript protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of reproductive system tumors and CNS tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 161

15 This gene is expressed primarily in adipose cell and to a lesser extent in liver and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: obesity and liver
20 disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adipose cell, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipose cells, liver, and
25 prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of obesity and liver disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 162

35 The translation product of this gene shares sequence homology with yeast ubiquitin activating enzyme homolog which is thought to be important in protein posttraslation processing.

This gene is expressed primarily in stromal cell and to a lesser extent in retina, H. Atrophic Endometrium, colon carcinoma and myeloid progenitor cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of stromal cell development, neuronal growth disorders and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., retinal cells, endometrium, colon, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ubiquitin-activating enzyme homolog indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of some type of tumors, fucosidosis and neuronal growth disorders.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 163

This gene is expressed primarily in primary breast cancer and hemangiopericytoma and to a lesser extent in adult brain and cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: breast cancer, leukemia and cerebellum disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of various tumors and disease involved in neural system.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 164**

The translation product of this gene shares sequence homology with proline rich proteins. Recently, another group has also cloned this gene, calling it CD84 leukocyte antigen, a new member of the Ig superfamily. (See Accession No. U82988, see also, Blood 90 (6), 2398-2405 (1997).)

- 10 This gene is expressed primarily in Weizmann olfactory tissue and osteoclastoma and to a lesser extent in anergic T-cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: ostsis and immune
15 disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., olfactory tissue, bone, and
20 blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 25 The tissue distribution and homology to the Ig superfamily indicate that the protein product of this clone is useful for treatment of osteoporosis, autoimmune disease, and other immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 165

- 30 This gene is expressed primarily in atrophic endometrium and colon cancer and to a lesser extent in some fetal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors. Similarly,
35 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, colon, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumors, specifically endometrium and colon tumors.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 166

This gene is expressed primarily in human primary breast cancer and to a lesser extent in activated monocyte. Although the predicted signal sequence is identified in Table 1, other upstream sequences are also relevant. Preferred polypeptide fragments comprise
15 the amino acid sequence: VTQPKHLSASMGGSEIPFSFYYPWELAXXPXVRISWRRGHFHG QSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQSVYFCRVELDTRRSG (SEQ ID NO: 641), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,
25 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in
30 healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 167

35 This gene is expressed primarily in fetal tissues and to a lesser extent in adult lung. This gene has also been mapped to chromosomal location 9q34, and thus, can be used as a marker for linkage analysis for chromosome 9.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryo tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissues, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 168

The translation product of this gene shares sequence homology with Ig Heavy Chain which is thought to be important in immune response.

This gene is expressed primarily in prostate cancer tissue specifically

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate, tissue and cells of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 169

The translation product of this gene shares sequence homology with cytosolic acyl coenzyme-A hydrolase, which is thought to be important in neuron-specific fatty acid metabolism. The gene represented by this contig has since been published by Hajra and colleagues (GenBank Accession No. U91316).

This gene is expressed primarily in human pituitary gland and to a lesser extent in colorectal cancer tissue. This gene has also been observed in the LNCAP cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hyperlipidemias of familial and/or idiopathic origins. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly blood, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pituitary and colon, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to rat cytosolic acyl coenzyme-A hydrolase indicate that polynucleotides and polypeptides corresponding to this gene are useful for the detection or treatment of hyperlipidemia disease states by virtue of the ability of specific drugs to activate the enzyme.

FEATURES OF PROTEIN ENCODED BY GENE NO: 170

The translation product of this gene shares sequence homology with a *Caenorhabditis elegans* gene which is thought to be important in organism development.

This gene is expressed primarily in human synovial sarcoma tissue, bone marrow, and to a lesser extent in human brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of bone, specifically synovial sarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, connective tissues and possibly immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, bone marrow, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another

tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution and homology to *Caenorhabditis elegans* indicate that polynucleotides and polypeptides corresponding to this gene are useful as a diagnostic and/or therapeutic modality directed at the detection and/or treatment of connective tissue sarcomas or other related bone diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 171

- 10 The translation product of this gene shares sequence homology with beta1-6GlcNAc transferase which is thought to be important in the transfer and metabolism of beta1-6, N-acetylglucosamine. This gene product has previously been shown to suppress melanoma lung metastasis in both syngeneic and nude mice, decreased invasiveness into the matrigel, and inhibition of cell attachment to collagen and laminin
15 without affecting cell growth.

This gene is expressed primarily in human testes and prostate tissues, and to a lesser extent in kidney, medulla, and pancreas.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at
25 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testes and other reproductive tissue, prostate, kidney, pancreas, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
30 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution and homology to beta1-6GlcNAc transferase indicate that the protein product of this clone is useful for the development of diagnostic and/or therapeutic modalities directed at the detection and/or treatment of cancer, the metastasis
35 of malignant tissue or cells. Defects in this potentially secreted enzyme may play a role in metastasis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 172

This gene is expressed primarily in fetal spleen and liver.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: immune disorders,
Wilm's tumor disease, hepatic disorders, and hematopoietic disorders. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the hematopoiesis and
immune systems, expression of this gene at significantly higher or lower levels may be
routinely detected in certain tissues and cell types (e.g., spleen and liver, and cancerous
and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
spinal fluid) or another tissue or cell sample taken from an individual having such a
15 disorder, relative to the standard gene expression level, i.e., the expression level in
healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for the treatment and identification of fetal defects
along with correcting diseases that affect hematopoiesis and the immune system.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 173

The translation product of this gene shares sequence homology with ret II
oncogene which is thought to be important in Hirschsprung disease and many types of
cancers.

25 This gene is expressed in multiple tissues including the lymphatic system, brain,
and thyroid.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for identification of the tissue(s) or cell type(s) present in a biological sample
and for diagnosis of diseases and conditions: Hirschsprung disease and multiple
30 cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful
in providing immunological probes for identification of the tissue(s) or cell type(s). For
a number of disorders of the above tissues or cells, particularly of the immune and
central nervous system, expression of this gene at significantly higher or lower levels
may be routinely detected in certain tissues and cell types (e.g., lymphoid tissue,
35 thyroid, and brain and other tissue of the nervous system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ret II oncogene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of various cancers. It would also be useful for the diagnosis and treatment of Hirschsprung disease. Preferred polypeptides of the invention comprise the amino acid sequence: MEAQQVNEAESAREQLQXLHDQIAGQKASKQELETelerLKQEFHYIEDLY RTKNTLQSRiKDRDEEIQKLrNQLTNKTLsnSSQSELENRLHQLTETLIQKQTMLESLSTEKNSL VFQLERLEQQMNSASGSSSNgSSINMSGIDNGEGTRLRNVPVLFNDTETNLAGMYGKVRKAAS
10 SIDQFSIRLGIFLRRYPiARVFViiYmALLHLWVMIVLLTYTPem HHDQPYGK (SEQ ID NO: 642).

FEATURES OF PROTEIN ENCODED BY GENE NO: 174

The translation product of this gene shares sequence homology with testis enhanced gene transcript which is thought to be important in regulation of human development.

This gene is expressed primarily in infant brain and to a lesser extent in a variety of other tissues and cell types, including the prostate, testes, monocytes, macrophages, dendritic cells, keratinocytes, and adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological, developmental, immune and inflammation disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, prostate, testes and other reproductive tissue, blood cells, keratinocytes, and adipocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to testis enhanced gene transcript indicate that the protein product of this clone is useful for diagnosis and treatment of disorders involving the developing brain and the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 175

This gene is expressed primarily in prostate and to a lesser extent in various other tissues, including placenta.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers, especially of the prostate. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
15 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of prostate disorders and cancer. It may also be useful for
20 the diagnosis and treatment of endocrine disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 176

The translation product of this gene shares sequence homology with *Sacchromyces cerevisiae* YNT20 gene which is thought to be important in
25 mitochondrial function.

This gene is expressed at a particularly high level in muscle tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases related to such tissues and cell types
30 including: muscle wasting diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuromuscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell
35 types (e.g., muscle and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the YNT20 gene indicate that this protein is useful for treatment and detection of neuromuscular diseases caused by loss of mitochondrial function. For example this gene or its protein product could be used in replacement therapy for such diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 177

This gene is expressed primarily in the brain and to a lesser extent in kidney, placenta, smooth muscle, heart and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuromuscular diseases, degenerative diseases of the central nervous system, and heart disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuromuscular system, central nervous system, and heart, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, kidney, placenta, muscle, heart and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

This gene or its protein product could also be used for replacement therapy for the above mentioned diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 178

The translation product of this gene shares sequence homology with caldesmon which is thought to be important in the cellular response to changes in glucose levels.

This gene is expressed primarily in multiple tissues including brain and retina.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: central nervous system disorders and retinopathy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the CNS disorders and retinopathy, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and retinal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to caldesmon indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of retinopathies.

FEATURES OF PROTEIN ENCODED BY GENE NO: 179

The translation product of this gene shares sequence homology with mouse fibrosin protein which is thought to be important in regulation of fibrinogenesis in certain chronic inflammatory diseases.

This gene is expressed primarily in amniotic cells and breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of breast cancer and abnormal embryo development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., amniotic cells, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to fibrosin indicate that the protein product of this clone is useful for treatment of breast cancer. This gene or its protein product could be used in replacement therapy for breast cancer. In addition the protein product of this gene is useful in the treatment of chronic inflammatory diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 180

This gene is expressed several infant tissues including brain and liver and various adult tissues including brain, lung, liver, testes, and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, brain cancer, lung cancer, liver cancer and cancers of the reproductive system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, hepatic system, and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, lung, liver, testes and other reproductive tissue, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene product indicates that the protein product of this clone is involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 181

This gene is expressed primarily in activated monocytes and to a lesser extent in melanocytes and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of immune system diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, melanocytes, and dendritic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 182

This gene is expressed primarily in placenta and several tumors of various tissue origin and to a lesser extent in normal tissues including liver, lung, brain, and skin,

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of cancers of all kinds. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
10 of the above tissues or cells, particularly of the central nervous system, respiratory system and skin, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, lung, brain and other tissues of the nervous system, and skin, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The high expression of this gene in multiple tumors indicates that the protein product of the clone may be involved in cell growth control and therefore would be
20 useful for treatment of certain cancers. Likewise molecules developed to block the activity of the protein product of this clone could be used to block its potential role in tumor growth promotion.

FEATURES OF PROTEIN ENCODED BY GENE NO: 183

25 The translation product of this gene shares sequence homology with the mouse Ndr1 gene which is thought to be important in cancer progression.

This gene is expressed multiple cell types and tissues including brain, lung, kidney, bone marrow, liver, and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of all types of cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune, and endocrine
35 systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, lung, kidney, bone marrow, liver and spleen, and cancerous and wounded

tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to Ndr1 gene, which is thought to be involved in cancer progression, indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of certain cancers. Likewise molecules developed to block the activity of the protein product of this clone could be used to block its potential role in tumor growth promotion.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 184

This gene is expressed primarily in early stage human brain and liver and to a lesser extent in several other fetal tissues.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain and liver cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the
20 central nervous system and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,
25 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 185

This gene is expressed primarily in infant and embryonic brain.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of degenerative nervous system disorders and brain cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 186

This gene is expressed primarily in multiple tissues including placenta, fetal lung, fetal liver, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of all types of cancers including liver, brain and lung. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, pulmonary system, and hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, lung, liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
1	HTTEZ21	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	11	582	1	582	177	313	1	18	19	22
1	HTTEZ21	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	197	1020	296	830	442	499	1	18	19	22
2	HGBW52	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	12	465	1	465	81	314	1	30	31	128
2	HGBW52	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	198	524	229	343	196	500	1	20	21	33
3	HCUFM41	97897 02/26/97 209043 05/15/97	ZAP Express	13	474	1	474	1	315	1	24	25	28
3	HCUFM41	97897 02/26/97 209043 05/15/97	ZAP Express	199	332	1	319	35	501	1	24	25	28

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
4	HCUFQ22	97897 02/26/97 209043 05/15/97	ZAP Express	14	314	1	298	122	122	316	1	34	35	64
5	HCUFV01	97897 02/26/97 209043 05/15/97	ZAP Express	15	613	1	613	30	30	317	1	18	19	21
6	HCUGA50	97897 02/26/97 209043 05/15/97	ZAP Express	16	356	1	356	239	239	318	1	22	23	39
7	HCUIM14	97897 02/26/97 209043 05/15/97	ZAP Express	17	414	185	414	278	278	319	1	26	27	33
8	HLD0U93	97897 02/26/97 209043 05/15/97	pCMV Sport 3.0	18	469	1	469	77	77	320	1	44	45	88
9	HEIAX07	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	19	550	1	550	129	129	321	1	21	22	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
9	HEIAX07	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	200	376	9	376		1	502	1	8	9	15
10	HSAXR76	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	20	741	55	741	190	190	322	1			27
11	HNGJJ68	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	21	991	1	991	62	62	323	1	30	31	64
11	HNGJJ68	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	201	1192	253	1137		409	503	1			19
12	HCFAW04	97897 02/26/97 209043 05/15/97	pSport1	22	653	1	653	64	64	324	1	30	31	196
12	HCFAW04	97897 02/26/97 209043 05/15/97	pSport1	202	589	1	513	109	109	504	1			29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	23	1486	596	1418	102	102	325	1	54	55	252
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	203	847	1	839	87	87	505	1	30	31	75
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	204	852	75	850		690	506	1			10
13	HTXEF04	209235 09/04/97	Uni-ZAP XR	205	1354	54	1354	100	100	507	1	33	34	207
14	HPMFD84	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	24	2323	1017	2059	1242	1242	326	1	21	22	68
14	HPMFD84	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	206	1378	113	1226	303	303	508	1	25	26	36
15	HE6DB26	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	25	683	1	683	304	304	327	1	30	31	84

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
15	HE6DB26	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	207	1166	281	884	567	567	509	1	18	19	19
16	HHFFL33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	26	2036	14	1959	214	214	328	1	20	21	36
17	HODBD33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	27	717	1	717	70	70	329	1	30	31	63
17	HODBD33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	208	697	2	697	33	33	510	1	31	32	32
18	HMDAE90	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	28	495	1	495	39	39	330	1	24	25	35
19	HOUAW01	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	29	556	1	556	116	116	331	1	19	20	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
20	HBJAE44	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	30	434	1	434	78	78	332	1	35	36	40
21	HCFME41	97897 02/26/97 209043 05/15/97	pSport1	31	715	1	715	87	87	333	1	30	31	111
21	HCFME41	97897 02/26/97 209043 05/15/97	pSport1	209	932	274	932	387	387	511	1	27	28	28
22	HOGCO71	97897 02/26/97 209043 05/15/97	pCMVSPORT 2.0	32	486	1	486	137	137	334	1	21	22	106
23	HOSEX08	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	33	725	1	725	436	436	335	1	30	31	50
23	HOSEX08	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	210	661	1	647	81	81	512	1	25	26	26

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
24	HSKNJ72	97897 02/26/97 209043 05/15/97	pBluescript	34	437	1	437	85	85	336	1	30	31	48
25	HEBEB69	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	35	943	1	943	196	196	337	1	30	31	41
25	HEBEB69	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	211	592	1	534	72	72	513	1	24	25	33
26	HE6EH18	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	36	604	1	604	375	375	338	1	20	21	76
26	HE6EH18	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	212	938	1	509		17	514	1	30	31	47
27	HSAUZ47	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	37	349	1	349		201	339	1	20	21	31

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
28	HSSDM73	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	38	672	1	672	22	22	340	1	38	39	42
29	HBMVK68	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	39	1908	135	1908	309	309	341	1	20	21	26
30	HMKDC66	97898 02/26/97 209044 05/15/97	pSport1	40	458	93	458	147	147	342	1	24	25	26
31	HMKCU94	97898 02/26/97 209044 05/15/97	pSport1	41	1153	500	1153	427	427	343	1	30	31	157
31	HMKCU94	97898 02/26/97 209044 05/15/97	pSport1	213	1079	502	896		739	515	1	23	24	43
32	HRDEW41	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	42	1983	1092	1983	27	27	344	1	11	12	520

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
32	HRDEW41	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	214	3791	2757	3357		2030	516	1			3
33	HTOIN06	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	43	1406	1	695		19	345	1	19	20	39
34	HBGDA21	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	44	1391	851	1153	74	74	346	1	30	31	234
34	HBGDA21	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	215	1334	822	1036		638	517	1	18	19	174
35	HFGAK75	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	45	1569	768	1569	14	14	347	1	19	20	169
35	HFGAK75	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	216	1511	770	1404	844	844	518	1	32	33	43

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
36	HHPBD40	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	46	1924	1	1681	62	62	348	1	19	20	43
37	HOVCL83	97898 02/26/97 209044 05/15/97	pSport1	47	475	252	396	141	141	349	1	37	38	78
38	HBCAY62	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	48	346	1	346	61	61	350	1	19	20	24
39	HBICM48	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	49	1366	882	1300	177	177	351	1	30	31	274
39	HBICM48	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	217	642	192	581		448	519	1			13
40	HLTCL35	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	50	1405	110	1404	61	61	352	1	30	31	47

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
40	HLTCL35	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	218	1241	1	1241	172	172	520	1	21	22	30
41	HLHCK50	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	51	504	207	485	222	222	353	1			3
42	HRSAN45	97899 02/26/97 209045 05/15/97	ZAP Express	52	777	1	214	113	113	354	1	24	25	52
43	HSNBB14	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	53	602	1	419	41	41	355	1	59	60	132
43	HSNBB14	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	219	1080	186	686	399	399	521	1	26	27	47
44	HMABL38	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	54	1749	222	1749	166	166	356	1	30	31	204

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
44	HMABL38	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	220	1258	149	1190	254	254	522	1	18	19	26
45	HSKDK47	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	55	1896	596	1614	650	650	357	1	33	34	47
46	HOSFH03	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	56	1753	555	1753	414	414	358	1	18	19	73
46	HOSFH03	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	221	1693	554	1693		526	523	1	25	26	58
47	HOGAV75	97899 02/26/97 209045 05/15/97	pCMVSPORT 2.0	57	1220	690	1024	128	128	359	1	30	31	102
47	HOGAV75	97899 02/26/97 209045 05/15/97	pCMVSPORT 2.0	222	1196	712	1163		1097	524	1			19

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
48	HFCAI74	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	58	1049	362	1049	335	335	360	1	33	34	48
49	HAGBI17	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	59	1776	854	1737	189	189	361	1	30	31	179
49	HAGBI17	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	223	1791	979	1791	1164	1164	525	1	18	19	40
50	HLFBC91	97899 02/26/97 209045 05/15/97	pBluescript SK-	60	443	1	443	164	164	362	1	21	22	25
51	HPRCA31	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	61	2888	1909	2888	90	90	363	1	30	31	224
51	HPRCA31	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	224	2517	1597	2517	1953	1953	526	1	18	19	57

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
52	HPRCE95	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	62	1851	1568	1736	139	139	364	1	30	31	349
52	HPRCE95	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	225	2424	299	2309		530	527	1	17	18	21
53	HHTLC66	97899 02/26/97 209045 05/15/97	ZAP Express	63	3542	883	3492	964	964	365	1	25	26	467
54	HMADI02	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	64	883	237	883	229	229	366	1	30	31	152
54	HMADI02	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	226	1080	242	1033	436	436	528	1	24	25	39
55	HPRCU93	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	65	1541	1	1541	236	236	367	1	30	31	373

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
55	HPRCU93	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	227	1336	4	1336	946	946	529	1	25	26	128
56	HSAXS65	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	66	732	41	698	163	163	368	1	18	19	83
56	HSAXS65	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	228	2043	1133	1756	1262	1262	530	1	20	21	82
57	HKTAG35	209011 04/28/97	Uni-ZAP XR	67	629	1	629	264	264	369	1			21
57	HMEFX42	97899 02/26/97 209045 05/15/97	Lambda ZAP II	229	540	25	536	227	227	531	1			20
58	HHFHN61	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	68	1751	375	1751	95	95	370	1	19	20	227
59	HCWEF90	97899 02/26/97 209045 05/15/97	ZAP Express	69	508	1	508	22	22	371	1	30	31	79

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
59	HCWEF90	97899 02/26/97 209045 05/15/97	ZAP Express	230	448	9	448		1	532	1	22	23	75
60	HHGCM20	97899 02/26/97 209045 05/15/97	Lambda ZAP II	70	245	1	245	93	93	372	1	1	2	51
61	HFRAU10	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	71	361	1	361	1	1	373	1	30	31	61
61	HFRAU10	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	231	407	1	407	210	210	533	1	17	18	60
62	HATDT67	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	72	713	8	713	169	169	374	1	30	31	40
62	HATDT67	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	232	830	190	580	329	329	534	1	28	29	39

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
63	HOUBG93	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	73	862	1	862	67	67	375	1	30	31	44
63	HOUBG93	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	233	932	138	905	287	287	535	1			2
64	HMWEX24	97900 02/26/97 209046 05/15/97	Uni-Zap XR	74	4602	4162	4525	730	730	376	1	30	31	203
64	HMWEX24	97900 02/26/97 209046 05/15/97	Uni-Zap XR	234	2786	2406	2739	2577	2577	536	1	22	23	36
65	HSGBA84	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	75	1255	1	1195	112	112	377	1	28	29	29
66	HTOCD52	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	76	475	1	475	13	13	378	1	30	31	136

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
66	HTOCD52	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	235	458	1	458	26	26	537	1			14
67	HTGCP16	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	77	465	25	299	74	74	379	1	33	34	41
68	HKIXR69	97900 02/26/97 209046 05/15/97	pBluescript	78	1907	1627	1730	26	26	380	1	30	31	468
68	HKIXR69	97900 02/26/97 209046 05/15/97	pBluescript	236	591	1	444	251	251	538	1			18
69	HETGJ09	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	79	1168	136	1168	267	267	381	1	20	21	29
70	HOBNC61	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	80	1285	132	1285	292	292	382	1	27	28	29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
71	HFFAH94	97900 02/26/97 209046 05/15/97	Lambda ZAP II	81	1290	768	1054	701	701	383	1	21	22	138
72	HBIAB95	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	82	684	1	684	119	119	384	1	30	31	74
73	HSQEL25	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	83	2024	1609	1953	200	200	385	1	30	31	521
73	HSQEL25	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	237	1286	391	959		1204	539	1	9	10	11
74	HEBEG68	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	84	931	14	537	85	85	386	1	25	26	137
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	85	825	59	802	66	66	387	1	30	31	186

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	238	734	1	734	1	1	540	1	37	38	108
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	239	809	80	794		294	541	1	15	16	106
76	HTXDU73	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	86	1238	36	918	17	17	388	1			1
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	87	1460	9	1458	166	166	389	1	53	54	299
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	240	2201	841	2080	507	507	542	1	43	44	136
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	241	1661	311	1520	390	390	543	1	35	36	424

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
78	HTEIY30	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	88	1395	567	1395	639	639	390	1	36	37	49
79	HSKNE46	97900 02/26/97 209046 05/15/97	pBluescript	89	1186	352	1186	540	540	391	1	49	50	61
79	HSKNE46	97900 02/26/97 209046 05/15/97	pBluescript	242	1146	329	1146	564	564	544	1	21	22	39
80	HPMFL27	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	90	1821	1203	1614	1503	1503	392	1	30	31	79
81	HMWWDN32	97900 02/26/97 209046 05/15/97	Uni-Zap XR	91	862	253	862	359	359	393	1	32	33	36
82	HPRAX55	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	92	696	349	696	98	98	394	1	30	31	180

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
82	HPRAX55	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	243	1350	265	1230	348	348	545	1	32	33	58
83	HHFFW36	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	93	1886	1	1759	197	197	395	1			21
84	HE2PL77	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	94	1774	742	1772	785	785	396	1	21	22	60
85	HSDFV29	209076 05/22/97	Uni-ZAP XR	95	2503	1	1648	206	206	397	1	32	33	152
85	HCQAV53	97901 02/26/97 209047 05/15/97	Lambda ZAP II	244	1529	72	911	191	191	546	1	20	21	33
86	HTPEG42	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	96	2801	418	2801	234	234	398	1	30	31	480
86	HTPEG42	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	245	1537	1	1537	125	125	547	1	21	22	367

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
87	HLHDR57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	97	1631	916	1631	1	1	399	1	1	2	423
88	HAUAV32	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	98	504	26	504	197	197	400	1	23	24	78
88	HAUAV32	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	246	506	1	499	183	183	548	1	32	33	77
89	HNEBI60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	99	1416	145	1416	456	456	401	1	18	19	74
89	HNEBI60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	247	1348	84	1348	363	363	549	1	21	22	47
90	HSJC116	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	100	2847	1	2847		2	402	1			20

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
91	HTSEL31	97901 02/26/97 209047 05/15/97	pBluescript	101	1394	608	1346	602	602	403	1	23	24	87
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	102	794	1	794	518	518	404	1	30	31	92
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	248	1766	42	1766	356	356	550	1	30	31	168
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	249	2664	47	1708		147	551	1	18	19	124
93	HODAS59	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	103	1544	898	1531	975	975	405	1			21
94	HE6CT48	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	104	871	106	871	248	248	406	1	34	35	174

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First of Secreted Portion	Last AA of ORF
94	HE6CT48	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	250	865	97	865	258	258	552	1	19	20	177
95	HMDAA61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	105	404	1	404	16	16	407	1	21	22	64
95	HMDAA61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	251	2082	852	2074	829	829	553	1	22	23	72
96	HAQBK61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	106	1542	506	1542	122	122	408	1	51	52	280
96	HAQBK61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	252	1482	508	1482		633	554	1	15	16	45
96	HCUHB01	209215 08/21/97	ZAP Express	253	834	1	834	82	82	555	1	40	41	251
97	HAQBF73	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	107	2327	1528	2327	465	465	409	1	30	31	284

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
97	HAQBF73	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	254	1508	885	1508		988	556	1			19
98	HAQBT94	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	108	1062	157	1062	172	172	410	1	28	29	187
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	109	2539	275	2501	903	903	411	1	30	31	237
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	255	2514	592	2431	176	176	557	1	30	31	217
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	256	2357	465	2288		1151	558	1	12	13	82
100	HLQAB52	97901 02/26/97 209047 05/15/97	Lambda ZAP II	110	1751	969	1751	4	4	412	1	46	47	192

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
100	HLQAB52	97901 02/26/97 209047 05/15/97	Lambda ZAP II	257	689	218	655	314	314	559	1	18	19	95
100	HEONN58	209119 06/12/97	pSport1	258	2377	5	2377	25	25	560	1	28	29	54
101	HCRAM28	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	111	1117	1	1117		1	413	1	19	20	21
101	HIBEK16	209627 02/12/98	Other	259	1193	69	1135	242	242	561	1	24	25	108
102	HE2BG03	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	112	1313	128	1313	271	271	414	1	30	31	51
102	HE2BG03	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	260	1262	26	1262	35	35	562	1	35	36	50
103	HEBDJ82	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	113	1654	553	1654	709	709	415	1			32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	114	1171	540	1171	337	337	416	1	30	31	163
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	261	1179	626	1161	335	335	563	1	30	31	253
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	262	1162	629	1131	942	942	564	1			18
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	115	842	373	800	100	100	417	1	65	66	174
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	263	735	290	735			565	1			
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	264	783	416	783		413	566	1	33	34	73

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	116	1640	187	1470	581	581	418	1	30	31	50
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	265	1638	301	1405	119	119	567	1	30	31	263
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	266	1455	148	1188	438	438	568	1	24	25	70
107	HE6DK18	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	117	952	418	906	499	499	419	1	28	29	120
108	HEBEK93	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	118	1256	21	1079	301	301	420	1	30	31	159
108	HEBEK93	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	267	1086	25	1050	227	227	569	1	23	24	34

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	119	1143	171	1051	175	175	421	1	50	51	154
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	268	1003	21	1003	115	115	570	1	34	35	104
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	269	1234	174	1015	232	232	571	1	27	28	132
110	HSXBL78	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	120	1782	1	1720	138	138	422	1	32	33	204
111	HOEAW81	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	121	610	18	609	50	50	423	1	30	31	67
111	HOEAW81	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	270	574	1	566	337	337	572	1	27	28	32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
112	HOEAP41	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	122	526	185	375	143	143	424	1	21	22	25
113	HEAAR60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	123	2081	1179	1976	48	48	425	1	30	31	299
113	HEAAR60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	271	1731	889	1626	886	886	573	1	18	19	28
114	HTXGS75	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	124	1717	764	1640	76	76	426	1			13
115	HOVBA03	97902 02/26/97 209048 05/15/97	pSport1	125	804	1	804	145	145	427	1	15	16	198
115	HOVBA03	97902 02/26/97 209048 05/15/97	pSport1	272	1320	77	637	280	280	574	1	22	23	40

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
116	HGBGK76	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	126	431	1	431	73	73	428	1	38	39	47
116	HGBGK76	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	273	515	1	515	43	43	575	1	20	21	30
117	HBMUW78	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	127	3752	3465	3752	748	748	429	1	30	31	370
117	HBMUW78	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	274	2995	2738	2995	2777	2777	576	1	18	19	29
118	HASAS24	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	128	1144	669	1144	896	896	430	1			30
119	HSIDN55	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	129	1830	1234	1830	1265	1265	431	1			24

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
120	HGBGZ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	130	1864	1505	1741	1578	1578	432	1	37	38	53
121	H6EBJ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	131	2041	1	1214	46	46	433	1	35	36	176
121	H6EBJ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	275	1990	8	1128	71	71	577	1	16	17	92
122	HOECP43	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	132	2012	853	1986	1127	1127	434	1	22	23	77
123	H2CBV31	97902 02/26/97 209048 05/15/97	pBluescript SK-	133	1669	670	1632	962	962	435	1	25	26	32
124	HPCAD23	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	134	1565	281	1565	274	274	436	1	25	26	30

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
125	HSPAG15	97902 02/26/97 209048 05/15/97	pSport1	135	2007	1101	2007	1124	1124	437	1	39	40	69
126	HELGH31	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	136	1291	1	1180	107	107	438	1			19
127	HUSHH48	97902 02/26/97 209048 05/15/97	Lambda ZAP II	137	1906	1	1906	184	184	439	1	30	31	43
127	HUSHH48	97902 02/26/97 209048 05/15/97	Lambda ZAP II	276	2436	572	2436	726	726	578	1	30	31	42
128	HLYAU95	97902 02/26/97 209048 05/15/97	pSport1	138	1935	1044	1794	1183	1183	440	1	18	19	33
129	HHSCV65	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	139	1446	572	1347	585	585	441	1	25	26	53

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
130	HTTAD57	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	140	1109	639	1109	676	676	442	1	24	25	64
131	HEBGA37	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	141	497	9	497	95	95	443	1			34
132	HEBFU93	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	142	269	1	269	1	1	444	1	30	31	89
132	HEBFU93	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	277	782	408	781		571	579	1	31	32	70
133	HSGSC60	97902 02/26/97 209048 05/15/97	Lambda ZAP II	143	1269	55	1262	55	55	445	1	25	26	350
134	HPMGD24	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	144	1944	97	1871	306	306	446	1	16	17	49

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
135	HPTVC60	97902 02/26/97 209048 05/15/97	pBluescript	145	1021	526	1021	74	74	447	1	30	31	278
135	HPTVC60	97902 02/26/97 209048 05/15/97	pBluescript	278	961	524	961	545	545	580	1	23	24	110
136	HSKNE18	97902 02/26/97 209048 05/15/97	pBluescript	146	1285	5	1285	116	116	448	1	30	31	199
136	HSKNE18	97902 02/26/97 209048 05/15/97	pBluescript	279	1228	9	1228	324	324	581	1	26	27	30
137	HMWIF35	97902 02/26/97 209048 05/15/97	Uni-Zap XR	147	1386	169	1272	165	165	449	1	30	31	258
137	HMWIF35	97902 02/26/97 209048 05/15/97	Uni-Zap XR	280	1327	169	1208	160	160	582	1	23	24	71

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
138	HMWGI25	97902 02/26/97 209048 05/15/97	Uni-Zap XR	148	2098	721	2044	784	784	450	1	18	19	87
139	HSKGF03	97902 02/26/97 209048 05/15/97	pBluescript	149	1847	1689	1847	241	241	451	1	33	34	315
139	HSKGF03	97902 02/26/97 209048 05/15/97	pBluescript	281	799	1	799		243	583	1	12	13	47
140	HMSKE75	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	150	1569	113	1517	417	417	452	1	21	22	52
141	HCMSH30	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	151	1540	538	1540	48	48	453	1	30	31	383
141	HCMSH30	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	282	2196	270	2196	294	294	584	1	32	33	39

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
142	HTWCB92	97902 02/26/97 209048 05/15/97	pSport1	152	1719	690	1575	6	6	454	1	52	53	186
143	HBMDM46	97902 02/26/97 209048 05/15/97	pBluescript	153	863	1	863	195	195	455	1	26	27	163
143	HBMDM46	97902 02/26/97 209048 05/15/97	pBluescript	283	1185	277	1166	621	621	585	1			19
144	HFAMG13	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	154	1101	1	512	40	40	456	1	21	22	46
145	HFXHL79	97903 02/26/97 209049 05/15/97	Lambda ZAP II	155	2031	669	2031	411	411	457	1	23	24	105
145	HFXHL79	97903 02/26/97 209049 05/15/97	Lambda ZAP II	284	1634	615	1485	878	878	586	1	20	21	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
146	HSNAK17	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	156	1981	1458	1809	1592	1592	458	1	23	24	70
146	HSNAK17	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	285	1795	1458	1749	1562	1562	587	1	33	34	69
147	HCFBC03	97903 02/26/97 209049 05/15/97	pSport1	157	915	45	912	22	22	459	1	22	23	155
147	HCFBC03	97903 02/26/97 209049 05/15/97	pSport1	286	858	46	858	224	224	588	1	30	31	77
147	HSJAP03	209139 07/03/97	Uni-ZAP XR	287	915	1	915	22	22	589	1	22	23	155
148	HSKGO26	97903 02/26/97 209049 05/15/97	pBluescript	158	2117	51	1422	32	32	460	1	23	24	332
149	HCQAV96	97903 02/26/97 209049 05/15/97	Lambda ZAP II	159	2395	1509	2382	1440	1440	461	1			5

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
150	HSNCC16	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	160	2120	1223	2108	1416	1416	462	1			14
151	HTLEF62	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	161	900	482	900	46	46	463	1	30	31	285
151	HTLEF62	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	288	1517	783	1517	1062	1062	590	1			24
152	HTLAD94	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	162	1003	1	1003	288	288	464	1	30	31	80
152	HTLAD94	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	289	3865	217	1195	281	281	591	1	16	17	38
153	HTSFQ12	97903 02/26/97 209049 05/15/97	pBluescript	163	2196	1607	2180	1611	1611	465	1	30	31	47

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
154	HE6FL83	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	164	1945	271	1840	299	299	466	1	63	64	96
154	HE6FL83	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	290	1910	279	1818	355	355	592	1	39	40	69
155	HTXFJ55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	165	2933	489	2871	258	258	467	1	30	31	399
155	HTXFJ55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	291	3276	486	2838		525	593	1	45	46	308
156	HJPCJ76	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	166	2243	343	2221		341	468	1			1
157	HLTED27	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	167	1816	1130	1816	284	284	469	1	31	32	273

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
157	HLTED27	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	292	1695	1098	1548	1306	1306	594	1			22
158	HMKBA64	97903 02/26/97 209049 05/15/97	pSport1	168	945	1	787	208	208	470	1	18	19	192
159	HNFIIP24	97903 02/26/97 209049 05/15/97	pBluescript	169	902	46	816	19	19	471	1	26	27	234
160	HCELB21	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	170	1883	798	1869	1001	1001	472	1	45	46	105
160	HCELB21	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	293	1501	438	1501	510	510	595	1			24
161	HAWBA28	97903 02/26/97 209049 05/15/97	pBluescript SK-	171	2100	1642	2100	1722	1722	473	1	23	24	32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
162	HSAAS44	97903 02/26/97 209049 05/15/97	pBluescript SK-	172	1930	187	1930	65	65	474	1	30	31	571
162	HSAAS44	97903 02/26/97 209049 05/15/97	pBluescript SK-	294	2683	183	2683	431	431	596	1			24
163	HAFAL73	97903 02/26/97 209049 05/15/97	pBluescript SK-	173	1509	962	1451	122	122	475	1	30	31	312
163	HAFAL73	97903 02/26/97 209049 05/15/97	pBluescript SK-	295	1454	961	1420	976	976	597	1			1
164	HSAWF26	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	174	3173	2197	2972	51	51	476	1	21	22	329
164	HSAWF26	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	296	828	52	828	305	305	598	1			8

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
165	HEAAL31	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	175	991	374	970	60	60	477	1	24	25	178
165	HEAAL31	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	297	2416	1387	2413	1473	1473	599	1	18	19	25
166	HFKFX55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	176	1290	499	1290		688	478	1	25	26	52
167	H2LAO11	97903 02/26/97 209049 05/15/97	pBluescript SK-	177	2290	1	2290	173	173	479	1	22	23	62
168	HPFDZ95	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	178	549	1	549	11	11	480	1	21	22	27
168	HPFDZ95	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	298	545	1	545	17	17	600	1	21	22	27

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
169	HPTTU11	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	179	1509	294	1352	92	92	481	1	30	31	339
169	HPTTU11	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	299	1530	385	1530	562	562	601	1	23	24	61
170	HCFAE79	97904 02/26/97 209050 05/15/97	pSport1	180	1316	985	1250	995	995	482	1	26	27	32
171	HTEDJ34	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	181	777	1	777	51	51	483	1	30	31	48
171	HTEDJ34	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	300	997	244	997	300	300	602	1	23	24	29
172	HODCW06	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	182	791	1	791	14	14	484	1	29	30	38

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
173	HFTAR26	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	183	1405	346	1405	575	575	485	1	20	21	61
174	H2MBF44	97904 02/26/97 209050 05/15/97	pBluescript SK-	184	1596	75	1596	131	131	486	1	24	25	346
174	H2MBF44	97904 02/26/97 209050 05/15/97	pBluescript SK-	301	2345	75	2345	233	233	603	1	56	57	69
175	HE8BI92	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	185	2293	355	2288	67	67	487	1	30	31	237
175	HE8BI92	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	302	2369	2	1946		60	604	1	9	10	24
176	HFTBR48	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	186	1212	462	1180	257	257	488	1	30	31	200

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
176	HFTBR48	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	303	1181	424	1149	663	663	605	1	23	24	35
177	HE9CM64	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	187	1605	770	1554	166	166	489	1	30	31	351
177	HE9CM64	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	304	1537	719	1515		787	606	1	43	44	130
178	HATAV51	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	188	1516	960	1516	8	8	490	1	30	31	265
178	HATAV51	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	305	1493	1	1261	54	54	607	1	18	19	23
179	HAQAF27	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	189	681	287	681		401	491	1			25

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
180	HCEEK08	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	190	1014	703	1014	360	360	492	1	30	31	159
180	HCEEK08	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	306	577	1	577		175	608	1			6
181	HAFU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	191	2779	2207	2630	1153	1153	493	1	30	31	279
181	HAFU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	307	2860	163	2860	21	21	609	1	30	31	232
181	HAFU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	308	876	275	876	302	302	610	1	32	33	34
182	HETBY74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	192	1923	30	1923	45	45	494	1	33	34	193

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
183	HTOAF35	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	193	2346	1160	2286	178	178	495	1	30	31	205
183	HTOAF35	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	309	2025	840	2025	971	971	611	1	18	19	21
184	HCRBX32	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	194	3054	2004	3054	434	434	496	1	11	12	147
184	HCRBX32	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	310	3026	1966	3026		2131	612	1			9
185	HEBGB80	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	195	907	152	907	297	297	497	1	30	31	64
185	HEBGB80	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	311	712	67	712	107	107	613	1	18	19	29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
186	HFAMH74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	196	1290	84	809	225	225	498	1	30	31	94
186	HFAMH74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	312	1289	785	1289	927	927	614	1	28	29	30

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988).

10 Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

15 Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1
20 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

25 In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
30 shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., +
35 or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

15 "Identity" per se has an art-recognized meaning and can be calculated using published techniques. (See, e.g.: (COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, A.M., ed., Oxford University Press, New York, (1988); BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed., Academic Press, New York, (1993); COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, (1994); SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, von Heinje, G., Academic Press, (1987); and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, (1991).) While there exists a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans. (Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988).) Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers," Martin J. Bishop, ed., Academic Press, San Diego, (1994), and Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988).

30 Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux, J., et al., Nucleic Acids Research (1984) 12(1):387 (1984)), BLASTP, BLASTN, FASTA (Atschul, S.F. et al., J. Molec. Biol. 215:403 (1990), Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711 (using the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981).)

35

When using any of the sequence alignment programs to determine whether a particular sequence is, for instance, 95% identical to a reference sequence, the parameters are set so that the percentage of identity is calculated over the full length of the reference polynucleotide and that gaps in identity of up to 5% of the total number of nucleotides in the reference polynucleotide are allowed.

A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990).) The term "sequence" includes nucleotide and amino acid sequences. In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB search of a DNA sequence to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, and Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, and Window Size=500 or query sequence length in nucleotide bases, whichever is shorter. Preferred parameters employed to calculate percent identity and similarity of an amino acid alignment are: Matrix=PAM 150, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, and Window Size=500 or query sequence length in amino acid residues, whichever is shorter.

As an illustration, a polynucleotide having a nucleotide sequence of at least 95% "identity" to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone, means that the polynucleotide is identical to a sequence contained in SEQ ID NO:X or the cDNA except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the total length (not just within a given 100 nucleotide stretch). In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to SEQ ID NO:X or the deposited clone, up to 5% of the nucleotides in the sequence contained in SEQ ID NO:X or the cDNA can be deleted, inserted, or substituted with other nucleotides. These changes may occur anywhere throughout the polynucleotide.

Further embodiments of the present invention include polynucleotides having at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone. Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the polynucleotides having at least 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity

will encode a polypeptide identical to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% "identity" to a reference polypeptide, is intended that the amino acid
5 sequence of the polypeptide is identical to the reference polypeptide except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the total length of the reference polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be
10 deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the
15 reference sequence or in one or more contiguous groups within the reference sequence.

Further embodiments of the present invention include polypeptides having at least 80% identity, more preferably at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by
20 the deposited clone. Preferably, the above polypeptides should exhibit at least one biological activity of the protein.

In a preferred embodiment, polypeptides of the present invention include polypeptides having at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98%, or 99% similarity to an amino acid
25 sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or
30 activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in
35 the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an

organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.

Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

5 Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988
10 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological
15 activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible
20 amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

25 Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form
30 are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show
35 substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make

phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

5 The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid
10 substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham
15 and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the
20 protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues
25 Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues,
30 where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino
35 acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

10 In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in
15 length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

20 Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, and 701 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly
25 recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the
30 deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, and 161 to the end of the coding
35 region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about"

includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

5 In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

10 Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if
15 it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is
20 meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred,
25 as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

30 Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular
35 locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

5 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the
10 polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

 Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of
15 immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86
20 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

 Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion
25 proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified,
30 would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol.
35 Chem. 270:9459-9471 (1995).)

 Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In

preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the claimed invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS,

293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes
5 known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention
10 can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic
15 cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can
20 be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using
25 fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to
30 mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross
35 hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage

analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the

present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute
5 biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags"
10 which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an
15 individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely
20 small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from
25 polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the
30 present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present
35 invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers
5 for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The
10 following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-
15 3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and
20 technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-
25 radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

30 A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I, 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the
35 subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20

millicuries of ^{99m}Tc . The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention could be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules

may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

5 A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells
10 from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

15 A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic
20 cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency
25 (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood
30 coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks
35 (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from

inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitis, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,

Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections.

5 A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, 10 Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide 15 of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide 20 of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

25 A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal 30 disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and 35 skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

Chemotaxis

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat

disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

5 A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or
10 small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural
15 receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell
20 membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

25 The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations,
30 polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

35 Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The

antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, circadian rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining

whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence
5 selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

10 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions
15 beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the
20 amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence
25 at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the
30 ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in
35 Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the

amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
5 least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
10 least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a
15 polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in
20 the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1;
25 and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining
30 whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of
35 polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an

amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

5 Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in
10 said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained
15 in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a
20 sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample
25 obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid
30 sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

35 Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least

90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated

polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of
5 illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

10 Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For
15 example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
20	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
25	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 30 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. 35 The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation

of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors
5 contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue,
10 Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the
15 corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone
20 identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited
25 sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.
30 The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as
35 those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection

agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μ l of reaction mixture with 0.5 μ g of the above cDNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 μ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to

remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

5 This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

10

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X.,
15 according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by,
20 among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is
25 then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are
30 mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5'
35 end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of

conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on
5 either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

10 A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product
15 into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

20 The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are
25 identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The
30 cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by
35 centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic

agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high
5 affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with
10 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in
15 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4° C or frozen at -80° C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number XXXXXX.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence,
25 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and
30 XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible
35 enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

- 5 The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

 Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at
10 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

- 15 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- 20 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

- Following high speed centrifugation (30,000 xg) to remove insoluble particles,
25 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

- To clarify the refolded polypeptide solution, a previously prepared tangential
30 filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a

stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem
5 columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0
10 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from
15 Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus

20 Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and
25 Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated
30 homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription,
35 translation, secretion and the like, including a signal peptide and an in-frame AUG as

required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μ g of a plasmid containing the polynucleotide is co-transfected with 1.0 μ g of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One μ g of BaculoGold™ virus DNA and 5 μ g of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μ l of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μ l Lipofectin plus 90 μ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μ Ci of 35 S-methionine and 5 μ Ci 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

25 **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

35 Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden),

pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., *J. Biol. Chem.* 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., *Biochem. et Biophys. Acta*, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., *Biotechnology* 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., *Biochem J.* 227:277-279 (1991); Bebbington et al., *Bio/Technology* 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., *Molecular and Cellular Biology*, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., *Cell* 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the

naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested
5 with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid
10 pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μ g of the expression plasmid pC6 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that
15 confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri
20 dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 -
25 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins.
30 These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the
35 polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having

more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in

5 Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

10 For example, if pC4 (Accession No.209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that
15 the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a
20 heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACCTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAAACC
25 CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
30 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA
35 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

10 In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

30 Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody

whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

5 It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of
10 recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art.
15 (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

20

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in
25 Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well
30 (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml
35 DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

5 Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of

10 transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off

15 PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (see below) with 2mm glutamine and 1x penstrep.

20 (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B

25 adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

30 It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an

35 activity in a particular assay.

HGS-CHO-5 medium formulation:**Inorganic Salts**

CaCl ₂ (anhyd)	116.6 mg/L
CuSO ₄ ·5H ₂ O	0.00130
Fe(NO ₃) ₃ ·9H ₂ O	0.050
FeSO ₄ ·7H ₂ O	0.417
KCl	311.80
MgCl ₂	28.64
MgSO ₄	48.84
NaCl	6995.50
NaHCO ₃	2400.0
NaH ₂ PO ₄ ·H ₂ O	62.50
Na ₂ HPO ₄	71.02
ZnSO ₄ ·7H ₂ O	.4320

5 Lipids

Arachidonic Acid	.002 mg/L
Cholesterol	1.022
DL-alpha-Tocopherol-Acetate	.070
Linoleic Acid	0.0520
Linolenic Acid	0.010
Myristic Acid	0.010
Oleic Acid	0.010
Palmitic Acid	0.010
Palmitic Acid	0.010
Pluronic F-68	100
Stearic Acid	0.010
Tween 80	2.20

Carbon Source

D-Glucose	4551 mg/L
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Amino Acids

L- Alanine	130.85 mg/ml
L-Arginine-HCL	147.50
L-Asparagine-H ₂ O	7.50
L-Aspartic Acid	6.65
L-Cystine-2HCL-H ₂ O	29.56
L-Cystine-2HCL	31.29
L-Glutamic Acid	7.35
L-Glutamine	365.0
Glycine	18.75
L-Histidine-HCL-	52.48

H ₂ O	
L-Isoleucine	106.97
L-Leucine	111.45
L-Lysine HCL	163.75
L-Methionine	32.34
L-Phenylalanine	68.48
L-Proline	40.0
L-Serine	26.25
L-Threonine	101.05
L-Tryptophan	19.22
L-Tyrosine-2Na- 2H ₂ O	91.79
L-Valine	99.65

Vitamins

Biotin	0.0035 mg/L
D-Ca Pantothenate	3.24
Choline Chloride	11.78
Folic Acid	4.65
i-Inositol	15.60
Niacinamide	3.02
Pyridoxal HCL	3.00
Pyridoxine HCL	0.031
Riboflavin	0.319
Thiamine HCL	3.17
Thymidine	0.365
Vitamin B ₁₂	0.680

Other Components

HEPES Buffer	25 mM
Na Hypoxanthine	2.39 mg/L
Lipoic Acid	0.105
Sodium Putrescine-2HCL	0.081
Sodium Pyruvate	55.0
Sodium Selenite	0.0067
Ethanolamine	20uM
Ferric Citrate	0.122
Methyl-B-Cyclodextrin complexed with Linoleic Acid	41.70
Methyl-B-Cyclodextrin complexed with Oleic Acid	33.33
Methyl-B-Cyclodextrin complexed with Retinal Acctate	10

5

Adjust osmolarity to 327 mOsm

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>ISRE</u> <u>Ligand</u>	<u>JAKs</u>				<u>STATs</u>	<u>GAS(elements) or</u>
		<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>		
5	<u>IFN family</u>						
	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS
	(IRF1>Lys6>IFP)						
	IL-10	+	?	?	-	1,3	
10	<u>gp130 family</u>						
	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS
	(IRF1>Lys6>IFP)						
	IL-11(Pleiotrohic)	?	+	?	?	1,3	
15	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
20	<u>g-C family</u>						
	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP
	>>Ly6)(IgH)						
25	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
30	<u>gp140 family</u>						
	IL-3 (myeloid)	-	-	+	-	5	GAS
	(IRF1>IFP>>Ly6)						
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
35	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	GAS(B-
40	CAS>IRF1=IFP>>Ly6)						
	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
45	PDGF	?	+	+	-	1,3	
	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCG
AAATGATTTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':CTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAATG
ATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
CTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTTCTCCGC
CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGC
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
TGCAAAAAGCTT:3' (SEQ ID NO:5)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a

neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using
5 SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

10 Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be
15 substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

20 **Example 13: High-Throughput Screening Assay for T-cell Activity.**

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS
25 signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-
30 SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

35 Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI

+ 10% serum with 1% Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

5 During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

10 The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

15 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

20 After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

25 The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophane covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material
30 for repeating the assay on a specific well if desired.

As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat pheochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)
5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

20

Example 16: High-Throughput Screening Assay for T-cell Activity

NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class I MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating diseases. For example, inhibitors of NF- κ B could be used to treat those diseases
5 related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
10 5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)
15 PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:
20 5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC
ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCCA
TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT
AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTC
CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:
25 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not
30 preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the

NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 μ l of 2.5x dilution buffer into Optiplates containing 35 μ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4

15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular

signaling even which has resulted in an increase in the intracellular Ca^{++} concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

5 The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In
10 addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the
15 cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

20 Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

25 Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 μl of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine
30 (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento,
35 CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are

used to cover the Loprodyn Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

- To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyn plates (20,000/200ml/well) and cultured overnight in complete medium.
- 5 Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim
- 10 (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation,
- 15 the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

- Generally, the tyrosine kinase activity of a supernatant is evaluated by
- 20 determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 25 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂⁺ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
- 30 components gently and preincubate the reaction mix at 30°C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction
- 35 mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This

allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as
5 above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
10 tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or compliment to the assay of protein tyrosine
15 kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
20 Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then
25 rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C
30 until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts
35 filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

10

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products is then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals is identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera
5 (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and
10 translocations. These alterations are used as a diagnostic marker for an associated disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

15 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

20 For example, antibody-sandwich ELISAs are used to detect soluble polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the
25 polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

30 Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

35 Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on

the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

5 The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for
10 purposes herein is thus determined by such considerations.

 As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 $\mu\text{g/kg/day}$ to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and
15 most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 $\mu\text{g/kg/hour}$ to about 50 $\mu\text{g/kg/hour}$, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes
20 and the interval following treatment for responses to occur appears to vary depending on the desired effect.

 Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal
25 patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

30 The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al.,
35 Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric

acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; 5 EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

10 For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the 15 formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the 20 carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that 25 enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or 30 immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, 35 poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of

about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g.,
5 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized
10 formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or
15 more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the
20 present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by
25 administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

30 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

5 For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

10

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin, is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

25 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to

35

transform bacteria HB 101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

5 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

10 Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the
15 titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is being produced.

20 The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

25 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Human Genome Sciences, Inc. et al.

(ii) TITLE OF INVENTION: 186 Human Secreted Proteins

10 (iii) NUMBER OF SEQUENCES: 644

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.

15 (B) STREET: 9410 Key West Avenue

(C) CITY: Rockville

20 (D) STATE: Maryland

(E) COUNTRY: USA

(F) ZIP: 20850

25

(v) COMPUTER READABLE FORM:

30 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 6.2

35 (D) SOFTWARE: ASCII Text

40 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: March 6, 1998

45 (C) CLASSIFICATION:

50 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

55

(viii) ATTORNEY/AGENT INFORMATION:

- 5 (A) NAME: A. Anders Brookes, Esq.
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PS002.PCT

10

(vi) TELECOMMUNICATION INFORMATION:

- 15 (A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8439

20

(2) INFORMATION FOR SEQ ID NO: 1:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 733 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG 60
AATTCGAGGG TGCACCGTCA GTCTTCTCTT TCCCCCAAA ACCCAAGGAC ACCCTCATGA 120
35 TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCCGTAGG 180
TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG 240
AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT 300
40 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG 360
AGAAAACCAT CTCCAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC 420
45 CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT 480
ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA 540
CCACGCCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCTT CTACAGCAAG CTCACCGTGG 600
50 ACAAGAGCAG GTGGCAGCAG GGGAAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC 660
ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCGC 720
55 GACTCTAGAG GAT 733

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

10 Trp Ser Xaa Trp Ser
1 5

15

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCGCCTCGAG ATTTCCCCGA AATCTAGATT TCCCCGAAAT GATTTCCTCG AAATGATTTC 60

30 CCGAAATAT CTGCCATCTC AATTAG 86

35 (2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

45 GCGGCAAGCT TTTTGCAAAG CCTAGGC 27

50 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

60 CTCGAGATTTC CCCCCGAAATC TAGATTTCCT CGAAATGATT TCCCCGAAAT GATTTCCTCG 60

AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120
GCCCCTAACT CCGCCAGTT CCGCCCATTC TCCGCCCCAT GGCTGACTAA TTTT TTTTAT 180
5 TTATGCAGAG GCCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240
TTTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCGCTCGAGG GATGACAGCG ATAGAACCCC OG 32

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCGAAGCTTC GCGACTCCCC GGATCCGCCT C 31

40

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGGGACTTTC CC 12

55

(2) INFORMATION FOR SEQ ID NO: 9:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCGGCCTCGA GGGGACTTTC CCGGGGACTT TCCGGGGACT TTCCGGGGACT TTCCATCCTG 60
 10 CCATCTCAAT TAG 73

15 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

25 CTCGAGGGGA CTTTCCCGGG GACTTTCCGG GGACTTTCCG GGACTTTCCA TCTGCCATCT 60
 CAATTAGTCA GCAACCATAG TCCCGCCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 120
 CAGTTCCGCC CATCTCCGC CCCATGGCTG ACTAATTTTT TTTATTTATG CAGAGGCCGA 180
 30 GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG 240
 CTTTTGCAAA AAGCTT 256

35

(2) INFORMATION FOR SEQ ID NO: 11:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCACGAGGT AATTTCTACC AGAAATTTCC AGAGCATTAT GTAGGTAGAA AAAAATGCAA 60
 50 GCAAGCTGTT AAAGATCTTG GATCCCATTA TATAGTATGT ATAGCTGAAA TCTGTAATTC 120
 AATCACTTTT TCTCTTTTAT CCTCTAACCA AAAAATGTGT TAATTTTGCA TCCCAAATGT 180
 TTTTAATCTT TGTATATTTT TTAAAAATCC TTTTCTCCTC ATCATTGCCT TTTTGTGGT 240
 55 TGTAATAGA CTTACTTGCA CTTTGAAGAT GAGTTACTCC TTGTATCTT ACAAATATGT 300
 GATATGGTAA TTTTCATAAC AGATGTCAGT TTTGAACCAA GAATTGGTGA TTTGTTTATA 360
 60 AGAAAAAAC TGGCTTCATT TCTGTGAAAT TGCTCTTGA AAATTTCTTT TTACACGTGT 420

5 AAGCCAACTG AGATACCGTG ATGGTGTGGA TTCTTTTCAA TGATGCTTAC CATCTATTTT 480
AGCCACTGAG CCTTTTATTA TTGTCTATT TGTAAGTTT ATTTGTCTTA ACTCATTTAA 540
TAAATATACT GTTTATCTGT TTCTGAAAAA AAAAAAAAAA AA 582

10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GT TTGGGGT GAGGCCGAGC TGCTGCGGGG CTTCGTCGCC GGCCAGGACA CAGCTACTCG 60
CACGGCGGCG GCGCCTGGCT ATGATGTTCC TCACCCAGGG CGGGCCTCTG CCCTCTACTC 120
25 GTGCCAGGCC CACTTGCCAG GCAGGAGCCC TCCCCAAGCC TTCAGGGCTG CTCGGAGTCA 180
CCTGTGGAA TGGACTAAAA GGACCCTTGT GTGGGAACAG GTGCTCCCA AACACCCTGC 240
TGCTGGCTGC CAGGCAGGCC CTCTGGAAGG GAAGGGGCG GACTCATCAG GACCTCCCTG 300
30 GACCCCTGCA GGGCAGGCAG CTTGGGCCCC AGCCCAAGCA TTGGGCTCTG CTGCCCCCAA 360
GGGACAGGA AGCCTCTTGG GCCTCTTCCC TTCTTGACA AGGCCCCCTG CCTTTGCCTC 420
35 ACATAAACTG TACAGTATTT TCATTAAAG CCTCTTTCAT AAAAA 465

40 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

50 ATGCAATTC TGCTCACAGC CTTCTGTGTG GTGCCACTTC TGGCTCTTTG TGATGTCCCC 60
ATATCCCTAG GCTTCTCCCC CTCCTAGAAG GGCTTCTTGA TAGATTAGAA AATAAGAATG 120
AGTGACATTT CCTATGTGCA TATAAGAAGG AGCCACAAGA CATGTCTTTT AAATAAAAGG 180
55 ACAGTGCCA TCCTTTTAGC TGCCGAATAG AACCTTGGTC TCATCCTCCT GGAGCTAGGC 240
CTTTAAACA GCTTCTGTGT TTCTCATTTG TCTCAGTGT TTGCCAGGT TTTATCGGAA 300
60 AGATAATGTT CCGTTTAAAA TATTTCTTAA TGAGGCCGGG CGTGGTGGCT CAGCCTGTA 360

ACCCTAGCAM TTGGGGGCTG AGCGGGTGGA TCACGAGGTC AGGAGATCGA GACCATCCTG 420
5 GSTAACATGG TGAAACCCCG TCTCTACTAA AAATACAAAA AAAAAAAAAA AAAA 474

10 (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

20 TTATGTTGGG GAGCAAGACC TGATAGCCAG CCTTTACATG GGAGTATAAT TCTGTCCTCC 60
ATCTCATAAG CCCAGTACC TGAGCCAGAA TGATTATAAC CAACCACACT GTCTCTTTAT 120
CATGGATGGC TTTAGCAGTA GGTATTTTTC ATCATTGCCA TTTGTAGCTC TACAGTGGTT 180
25 TATAGTAATT TCTCATCTTT TAAGTCTCTC CCTCAGTGCC TGTGTTATC AAATCATTC 240
CTCTCTCANG CAGTTGAGCT CTGCATTCTC CCYTATGGGG GAGAGCTGTG TTGGAGAGAG 300
AGAATATNAC TTCC 314
30

35 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 613 base pairs
 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

45 CTCATATTGC CGTCTGGCTA AAAGTGAACA TGCCATTGAT CAATCTGCTT TTATTATATT 60
ATGTTCTTAA TGGTGGCAAG CAAGACAAGA AGTAGAAAGA AAGATGGTGT AAGCTCAAGA 120
ACCCACTAAA TCTATCCTAT GGCCTGGGTT CACCCAGCCT GCTTTGTGGA TTTTGTCTCA 180
50 CTATAACAGA GCTCCCAAGG AGACTGCAGA GTCAGCTCCC TTAAGCACTG TAACTAAAGC 240
CTAACTCTTC CGTTCACCCC AACAATGTYC CCAGCTCATC CTCTTTCCCR AAGTCCCTTT 300
TCTGCCCCAG ATGCGAATTG CATTTAACTA ATCTCAAGT GAAATGTCCA CACAGRATTC 360
55 CATTTTAATT AGCATACCAT AGTTTMTGTG CAAATTTGCT TTCAGARGAC TCCCATTGCA 420
GCTGCTCAGA GACGCTAAWG GCAGGGCCTC TTGAWGCTTT CCCGATAGCT TTCAGCTGCA 480
60 ATAGCTCTTA GGCAGAATGC CATGAGCGTC CTGCCCAACT GTATTACTGG GGAACACCTG 540

ATTGGCTAGA AGTTGATCCT CCTGTAACTT TTCTGAGTTC TTTACATTTA CTCGTGAAAC 600
CCAAATATGC CAC 613

5

(2) INFORMATION FOR SEQ ID NO: 16:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCCCCCCCAT TGAACCTGG GCTGTGAAAG TTTTTCCTG TGTGGTCTG TCTGTGTGGC 60
GCCTGGTGTG TGGKTCCCAA CTCCTGTTGC AAAGTGGCAG CAGCCAATCA TGAAGCGCCC 120
TTATTTTTAG TTGCAGATGA CCAGGTCTCC CCCCCACAGC CTCTGTCTGG TCCCTCATTG 180
GTGAGTGGTC TGCCTGCCCA AGGAGCCTGA TTGGTGGGAA ATGGCATCAT CTAATATGAT 240
GGGAAGGCAT TTGGTCCTGG TTATGTTTAT TACAACATCA TTGCACTCTG GGAATCCAGT 300
CCCTGAAAAC GTAATTTGTG GTGTTACCAA AGGACCACAG GGGAAAAAAA AAAAAA 356

30

(2) INFORMATION FOR SEQ ID NO: 17:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GAAACTANAT CCCGGGGCTT TTAACNGGTA CTTGGGAAAT AAGTATTGGG TAATCACTAA 60
GNGGACATTG ACTGCACCAA ACCAAAGCTA TAGAAAGAAA TGATTGACTT TTTAAAATAT 120
ATTCACATTA ACTGTCCTAG GATACTTCTC TTGAGGCTTT GGAAAACATC TTCCTTGAAA 180
TTTGCATATC CACTCCAGTT CTGTCACCAA AGATTTTAAT CTTGAGATCG CAATTTCTCT 240
TCTCCCAGAA AAAAGTACTA CAACAGGCTC AAGGGATATG CTTTGGTGGT CAAGGGATTA 300
CACTATGGTT TTCCTTCTGT TCACAATGGT ATTTACAGGA GACCTTGTCA TCAGAGGACG 360
TACTGAACTA TCTTTATGAC TTTGGATTTG ATCAGAGGTT TAAAAAAA AAAA 414

55

60

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

10

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AATCACCATT GCAATACAAA TGATCTGCCT GGTGAATGYT GAGCTGTACC CCACATTCGT      60
CAGGAACYTC GGAGTGATGG TGTGTTCCCTC CCTGTGTGAC ATAGGTGGGA TAATCACCCC      120
CTTCATAGTC TTCAGGCTGA GGGAGGTCTG GCAAGCCTTG CCCCTCATTT TGTTCGCGGT      180
GTTGGGCCTG CTTGCCGCGG GAGTGACGCT ACTTCTTCCA GAGACCAAGG GGGTCGCTTT      240
GCCAGAGACC ATGAAGGACG CCGAGAACCT TGGGAGAAAA GCAAAGCCCA AAGAAAACAC      300
GATTTACCTT AAGGTCCAAA CCTCAGAACC CTCGGGCACC TGAGAGAGAT GTTTTGCGGC      360
GATGTCGTGT TGGAGGGATG AAGATGGAGT TATCCTCTGC AGAAATTCCT AGACGCCTTC      420
ACTTCTCTGT ATTCTTCCTC ATACTTGCTT ACCCCCCAAT TAATATCAG      469

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30

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

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40 CCCCCCCCCC CCCCCACACT TTCAGGAGTC ACCCCCCAGC ATTTGGGGTT GGGTTGGCCC      60
TACTCCAGCC TGGAGCTCCC TGAGGGAGCC TGCACTCCCT GCTCCCAATC CCCGCTACTG      120
GTGCAGGGAT GCAGCCTGGA GCTGGCGTCC TTGTTCTGGG CCTGCTGCTG CCGCCACCCC      180
45 AGAGCCCCAG CCTGTCTGA ATTGACATCA GTGCTTCCCT GAACTGCCTC CCCCACCCCT      240
GGGCATTATC CCAGGAAACT TTATGTTTTT TAGAAGCTAA GCAGCTGCTG GGAATCAGGG      300
50 ACTGGTGCAG GTAGGCTGAG TGGCAGCTCA GTCTAGAAG GTCTCTGAAG ATCTGGACTG      360
AGGACCTTGC TACTCCCCAA GCCAGAGCCC ATCAGCCAGG CCTGCTGTGA GCCACCTGCC      420
TGTGGAGTGC TGAGCTCAAC CAAAGGCTGG CAAGCTCTGG GCCTCATTTA AGGGATTTCTG      480
55 ATGAGCCGAT GGGCCCTGGA GGCAGCCCAT TAAAGCATCT GGCTCGTTTT TGAAAAAAA      540
AAAAA      550

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60

(2) INFORMATION FOR SEQ ID NO: 20:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TCTTGAAGAG TGTACAGTAC AGGATTATTA TAATGAAAGT TTATATCAAC AGGGTTTCGT 60
15 TGGCTCTGCA TATATTATAA GCAAAAGAGA TTGGTAAAGT GCCACAGTAT TCCAGATAAC 120
TTTTCAGTTG CGGCCTTTCT TCTCGTTCTT TAATTTGAAA CCTAGATACA TGCAGTAAAA 180
ACTAGGAGAA TGACTTTTAC CCTTGGGGAC AGCCAAGTTT TGTGATAAA CCTATTTCCT 240
20 AGCATGCCTT CAGGAAGTTG TGCCAGACCC TAGATTGTGA AGGACCCACT GTTCTTCTGT 300
TGTACGAGCT CCCTGAACCA TTGTTTCAGAG GACCAATGTC ACATCGCTTC ATGGGCATGG 360
25 NCCATGGGAG CATCTGGGTG ATAYCTGTCT ACAGTATTGG CTCTTCTGCG AGGCTGATAC 420
ACAAGGCCTC TCTTCCACAT GATCATTGTC AAACCTCCCC CAGCCCCTAC CATCCAATGT 480
GGAAGGAAAA CAAGAACTGC CTGAAGAAGA GTCCAAGCTA CAGATACACA GCGTGTGCAT 540
30 TGGCGCTGTC ACCTTCCTCC TCCCATTCT GTATCCTCAG AGATGCTGCG TGGATGTTTC 600
CTTAACCTCA GCTGACTTCC CTGTGAATGT CTAATGCTAG TTCAGGGCCT CCAGGCATTG 660
35 ATTTGTACAG TGTAATCC CAATGAGGCT TCTGTTATCA TTTGGTGTGC TTTYTCTGTC 720
ATTAAAAGAA ATGATTTTCC C 741

40

(2) INFORMATION FOR SEQ ID NO: 21:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 991 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCACGAGTC TCCCCTGGGG AAGTTTTTCT TTTTCAGGAG GGAGGAGGGC TTTCCCAGGT 60
AATGTGTCTA GAGTGTGGG CAGAAAATCT GGGACCACAC CACACCAGTT CTCTCCTTAA 120
55 TCCACGTCAT TTGCCTTCTA TCCCAGCTAT GTTTCAGTGT TCCTCTGGGT GTTTCGAAGA 180
GCAACAAGAA ATGAATAAAT CTCTGGTGAG TTGTTTATTT GTCTTCACT TTGTTTTACA 240
60 CTGTATTTTC TGAGTTTATG GGTGTCTGTG AATTAAAAAG GAAAAGTAGA AATAAGTAAA 300

ACTCAGGTTG AAGGAAATAT ACATAAATAA GATAAAGCTG ACCTGTAGAT ATAGCAGGTT 360
 ATAAAGCTTA GAGTTGTCTA AGTTGAGTGC AAATTTTCCT CTGATCTTTC TGATGCCGAA 420
 5 CAAAAAAGCA GTCATGTTTG TTATGTGATT GGAATGGAAC CCGAGAAGAG AGCATGCTGT 480
 GTTCTTGTGG GACAGGAAAG CTTGCGTGCA CCAAGTCTGA ACCACCACCT TCATGGTGAC 540
 10 ATAGATTATG TGCTGGAACA TATTTACAC CCGCTGGCA GTAAACACTT GTAGTGTGT 600
 GCAGTGAAA CGTCATCTT CCGCTAAAGC ACGCGTGT GTGCAGCGGA AATGGTCATC 660
 TGCTGCTAAA ACACAGCTTC CATCGTAATG TATGCTCCTT ACTCAAAGAG TGTGTTCCA 720
 15 AACAGCCTTT GGGAGGTCCT CCTGATTCA TGGATGAAAC CTGGAACATC TTGAGGACTG 780
 AGTTAACCAT AGGTCCTTAA ATAACCTCC ACACGTTTTT CTTAGTTTAT CTCTACATGC 840
 20 AGGGTGTGCA GCAGCCTGTT CAAAGTCATA TTTTCTGGGA AATATTTCCA GTGTTTATTT 900
 GCACCTTAGC CCACTCTGTG TAGCCTTATT TCTCTAAAC TCACCATTA TCTGAATAAT 960
 AGTCAAATTT AGGGGACTG TATTTGCCTT A 991
 25

(2) INFORMATION FOR SEQ ID NO: 22:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCACGCGTCC GGAATTCCTT TGAGGATCTT GGGCTATCTT TGACAGGGA TTCTTGCAAG 60
 40 TTGATGCTTT CTACAAGTGA ATATAGTCAG TCCCCAAGA TGGAGAGCTT GAGTTCTCAC 120
 AGAATTGATG AAGATGGAGA AAACACACAG ATTGAGGATA CGGAACCCAT GTCTCCAGTT 180
 45 CTCAATTCTA AATTTGTTCC TGCTGAAAAT GATAGTATCC TGATGAATCC AGCACAGGAT 240
 GGTGAAGTAC AACTGAGTCA GAATGATGAC AAAACAAAGG GAGATGATAC AGACACCAGG 300
 GATGACATTA GTATTTTAGC CACTGGTTGC AAGGGCAGAG AAGAAACGGT AGCAGAAGAA 360
 50 GTTGTATATG ATCTCACTTG TGATTCCGGG AGTCAGGCAG TTCCGTCACC AGCTACTCGA 420
 TCTGAGGCAC TTTCTAGTGT GTTAGATCAG GAGGAAGCTA TGGAAATTAA AGAACCCAT 480
 55 CCAGAGGAGG GGTCTTCAGG GTCTGAGGTG GAAGAAATCC CTGAGACACC TTGTGAAAGT 540
 CAAGGAGAGG AACTCAAAGA AGAAAATATG GAGAGTGTTC CGTTGCACCT TTCTCTGACT 600
 GAAACTCAGT CCAAGGGTT GTGTCTTCGG AGGCATCCAA AAAAAAAAAA AAA 653
 60

(2) INFORMATION FOR SEQ ID NO: 23:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

15	GGCAGGCTGA CGACCTGCAA GCCACAGTGG CTGCCCTGTG CGTGCTGCGA GGTGGGGGAC	60
	CCTGGGCAGG AAGCTGGCTG AGCCCCAAGA CCCCAGGGGC CATGGGCGGG GATCTGGTGC	120
	TTGGCCTGGG GGCCCTGAGA CGCCGAAAGC GCTTGCTGGA GCAGGAGAAG TCTCTRGCCG	180
20	GCTGGGCACT GGTGCTGGCA SGARCTGGCA TTGGACTCAT GGTGCTGCAT GCAGAGATGC	240
	TGTGGTTCGG GGGGTGCTCG GCTGTCAATG CCACTGGGCA CCTTTCAGAC ACACTTTGGC	300
	TGATCCCCAT CACATTCTCTG ACCATCGGCT ATGGTGACGT GGTGCCGGGC ACCATGTGGG	360
25	GCAAGATCGT YTGCTGTGC ACTGGAGTCA TGGGTGTCTG CTGCACAGCC CTGCTGGTGG	420
	CCGTGGTGGC CCGGAAGCTG GAGTTTAACA AGGCAGAGAA GCACGTGCAC AACTTCATGA	480
30	TGGATATCCA GTATACCAA GAGATGAAG AGTCCGCTGC CCGAGTGCTA CAAGAAGCCT	540
	GGATGTCTTA CAAACATACT CGCAGGAAG AGTCTCATGC TGCCCGCANG CATCAGCGCA	600
	ANCTGCTGGC CGCCATCAAC GCGTTCCGCC AGGTGCGGCT GAAACACCGG AAGCTCCGGG	660
35	AACAAGTGAA CTCCATGGTG GACATCTCCA AGATGCACAT GATCCTGTAT GACCTGCAGC	720
	AGAATCTGAG CAGCTCACAC CGGGCCCTGG AGAAACAGAT TGACACGCTG GCGGGGAAGC	780
40	TGGATGCCCT GACTGAGCTG CTTAGCACTG CCCTGGGGCC GAGGCAGCTT CCAGAACCCA	840
	GCCAGCAGTC CAAGTAGCTG GACCCACGAG GAGGAACCAG GCTACTTTCC CCAGTACTGA	900
	GGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCCAGCCCTG AACAAAGCAC CTCAAGTGCA	960
45	AGGACCAAAG GGGGCCCTGG CTTGGAGTGG GTTGGCTTGC TGATGGCTGC TGGAGGGGAC	1020
	GCTGGCTAAA GTGGGKAGGC CTTGGCCAC CTGAGGCCCC AGGTGGGAAC ATGGTCACCC	1080
50	CCACTCTGCA TACCTCATC AAAAACACTC TCACTATGCT GCTATGGACG ACCTCCAGCT	1140
	CTCAGTTACA AGTGCAGGCG ACTGGAGGCA GGA CTCTGG GTCCCTGGGA AAGAGGGTAC	1200
	TAGGGGCCCG GATCCAGGAT TCTGGGAGGC TTCAGTTACC GCTGGCCGAG CTGAAGAACT	1260
55	GGGTATGAGG CTGGGGCGGG GCTGGAGGTG GCGCCCCCTG GTGGGACAAC AAAGAGGACA	1320
	CCATTTTTC AGAGCTGCAG AGAGCACCTG GTGGGGAGGA AGAAGTGTA CTCACCAGCC	1380
60	TCTGCTCTTA TCTTTGTAAT AAATGTTAAA GCCAGAAAAA AATAAAAAA AAAAAAAAAA	1440

AACTCGAGGG GGGCCCRKAC CCAATCWCCC TATAGTAKAC GTANNN

1486

5

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CTTCGCCGTT	TCTCCTGCCA	GGGAGGTCC	CGGCTTCCCG	TGGAGGCTCC	GGACCAAGCC	60
CCTTCAGCTT	CTCCCTCCGG	ATCGATGTGC	TGCCGCCGCC	GCCGCCGCCG	TCCCGCGTCC	120
TTCCGTCTCT	GCTCCCGGGA	CCCGGCTCCG	CGCAGCCAGC	CAGCATGTCT	GGGATCAAGA	180
AGCAAAAGAC	GGAGAACCAG	CAGAAATCCA	CCAATGTAGT	CTATCAGGCC	CACCATGTGA	240
GCAGGAATAA	GAGAGGGCAA	GTGGTTGGAA	CAAGGGGTGG	GTTCGGAGGA	TGTACCGTGT	300
GGCTAACAGG	TCTCTCTGGT	GCTGGGAAAA	ACAACGATAA	GTTTTGCCCT	GGAGGAGTAC	360
TTGTCTCCCA	TGCCATCCCT	GTTAATTCCT	GGATGGGGAC	AATGTCCGTC	ATGGCCTTAA	420
CAGAAATCCC	CAGATGGCTT	CATGGCCCCC	AAAGCATGGA	AGGTCCTGAC	AGATTATTAC	480
AGGTCCTGTC	AGAAGAACTA	AGCCTTTGGT	CCAGAGTTTC	TTTCTGAAGT	GCTCTTTGAT	540
TACCTTTTCT	ATTTTTATGA	TTAGATGCTT	TGTATTAAAT	TGCTTCTCAA	TGATGCATTT	600
TAATCTTTTA	TAATGAAGTA	AAAGTTGTGT	CTATAATTAA	AAAAATATAT	ATATATATAC	660
ACACACACAT	ATACATACAA	AGTCAAACCT	AAGACCAAAT	CTTAGCAGGT	AAAAGCAATA	720
TTCTTATACA	TTTCATAATA	AAATTAGCTC	TATGTATTTT	CTACTGCACC	TGAGCAGGCA	780
GGTCCAGAT	TTCTTAAGGC	TTTGTTTGAC	CATGTGTCTA	GTTACTTGCT	GAAAAGTGAA	840
TATATTTTCC	AGCATGTCTT	GACAACTGT	ACTCTTCCAA	TGTCATTTAT	CAGTTGTAAA	900
ATATATCAGA	TGTGTCCTCT	TCTGTACAAT	TGACAAAAAA	AAAAATTTT	TTTCTCACT	960
CTAAAAGAGG	TGTGGCTCAC	ATCAAGATTC	TTCTGATAT	TTTACCTCAT	GCTGTACAAA	1020
GCCTTAATGT	TGTAATCATA	TCTTACGTGT	TGAAGACCTG	ACTGGAGAAA	CAAAATGTGC	1080
AATAACGTGA	ATTTTATCTT	AGAGATCTGT	GCAGCCTATT	TCTGTCACAA	AAGTTATATT	1140
GTCTAATAAG	AGAAGTCTTA	ATGGCCTCTG	TGAATAATGT	AACTCCAGTT	ACACGGTGAC	1200
TTTTAATAGC	ATACAGTGAT	TTGATGAAAG	GACGTCAAAC	AATGTGGCGA	TGTCGTGGAA	1260
AGTTATCTTT	CCCCTCTTT	GCTGTGGTCA	TTGTGTCTTG	CAGAAAGGAT	GGCCCTGATG	1320

60

	CAGCAGCAGC GCCAGCTGTA ATAAAAATA ATTCACTA TCAGACTAGC AAGGCACTAG	1380
	AACTGGAAAA GACCACAGAA AACAAAGAAT CCAACCCTTT CATCTTACAG GTGAACAAAC	1440
5	TGTGATGATG CACATGTATG TGTMTTGTA GCTGTGAGCA CCGTAACAAA ATGTAAATTT	1500
	GCCATTATTA GGAAGTGCTG GTGGCAGTGA AGAAGCACCC AGGCCACTTG ACTCCAGTC	1560
10	TGGTGCCCTG TCTACACCAG ACAACACAGG AGCTGGGTCA GATTCCTTC AGCTGCTTAA	1620
	CAAAGTTCCT CGAACAGAAA GTGCTTACAA AGTGCCTTC TCGGATACTG AAAGGTCGAG	1680
	TTTCTGAAC TGCACTGATT TTATTGCAGT TGAAAAAAA AAAAAGCTAT TCCAAAGATT	1740
15	TCAAGCTGTT CTGAGACATC TTCTGATGGC TTTACTTCCT GAGAGGCAAT GTTTTTACTT	1800
	TATGCATAAT TCATTGTTC CAAGGAATAA AGTGAAGAAA CAGCACCTTT TAATATATAG	1860
20	GTCTCTCTGG AAGAGACCTA AATTAGAAAG AGAAAAGTGT GACAATTTTC ATATTCTCAT	1920
	TCTTAAAAAA CACTAATCTT AACTAACAAA AGTTCTTTTG AGAATAAGTT ACACACAATG	1980
	GCCACAGCAG TTTGTCTTIA ATAGTATAGT GCCTATACTC ATGTAATCGG TTAICTACTA	2040
25	CTGCCTTTAA AAAAAAAC CAGCATATTT ATTGAAAACA TGAGACAGGA TTATAGTGCC	2100
	TTAACCGATA TATTTTGTGA CTAAAAAAT ACATTTAAAA CTGCTCTTCT GCTCTAGTAC	2160
30	CATGCTTAGT GCAATGATT ATTTCTATGT ACAACTGATG CTTGTCTTIA TTTTAATAAA	2220
	TTTATCAGAG TGAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	2280
	AAAAAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA	2323
35		

(2) INFORMATION FOR SEQ ID NO: 25:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

	GGCACGAGCC TGTGTGGTCA TGTTCCTCGT GGTGCAGTAC CTGACATGAG CCAGCCACGC	60
50	TCAGTGGCTG AACAGCATTC CCACAGCCTG CAAGTGTGTG TGTGTGTGAA AGAGAGAGGG	120
	GGGCCAGAG CCGCCTTTTG AAATGTTTGC CTGTCTGAAC TGTGAAGACA CTTGGGAGTG	180
55	ATTGTGGTCT AATTTC AAC CTGCTCTGTT TTCTGTGACA TCTTGGAGGG GAGCTAGTGC	240
	CACACCATGC GCGGTGCTTA GAAATGAAAA AGTCCCGGGT CTGTCTCTCT CACTCTCGCT	300
	CTCATGGGGG AGGGAAGAA TGGCTTTGGT GGCTTTGTTC ACACAGCTGA TGCCTGCTGG	360
60	GAAGGTGTCC ACAGTGAGCC TGTGTGCAGG ACTGTCCACA CGGTTACAC TTGTCACCAT	420

CAGGCCTTTC TGGTCCTGAT AGGGTGGAGC AAAAGTGGAA AGGAAAGGAA AGAGGCTTTT 480
 CTCACAGCCA TTATATTAAA TAGTAGGTCG ATTCACATCT CGTGCTCCTG GCCACCTTCC 540
 5 CCTGTGCCTC AGTGACATGT AGATGACTGA CTGCCAATAC TTGTCACCAT TCCCTGGAAG 600
 CAGCTACCTA GGGGAAACAA GATGTAGTGC TATTGCCGAT AACAAGTAAG ATTTTCCACA 660
 10 CTAAAAAAA AAAAAAAAAA AAA 683

15 (2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2036 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

25 CTGAGAAAGG AAAGCATTCG GATCTGCTGC AAAACACAT ATATCCATAA AGACTCATGT 60
 TATTCAGAAA ACAGATTGTG AACACAATCA CATTCGCATG AATCCTTTAA AAGGAAGAAG 120
 ACCTTAAAGT ATCTGCAAAT CTGAATTTCT ATTTATTCCT TCACTGAATA TAGAAACAAT 180
 30 GGTATCTGA TTATTAGAGA TATTATTTTG GATATGTTAC TTATTAACTT GCTATGGCTG 240
 GTAACCATGA TAAAGTCTGT TATTAATAAC AACATAATTC TTTTTTTAAA GAAGAAAAGC 300
 35 TTATTTTCA TTGACAGTGT ATAGATTTAT CTACTTAGTT GTGTTTGTCT ATTAGTGTTT 360
 TAATTTTTTT TTTAAGTTGA GTGTTTGATA AATTTTAAAG CCCTGTCCCC ACCTTGTTTT 420
 GAGTCCTGTG TTGACTACAG GTATATAGCY CAWTTTAAAA ATCCTAAAGC AAAAGAATTT 480
 40 TATTTATAAA AGAATCMAMC MGTGTCATGC ATGAGGCTGT GAAGTCAGAT ATTTAGTAAT 540
 AAAAGCAGCA GTGCCTTTTT TTGTATTTAC CCATTGACCC CCACCAAATG CAACTGTTTT 600
 45 ATATTAAGAA AATAGTAACA ATTTTAAAT CTCAGAGTAA AATCTATTTT ACTACATGCT 660
 TTTCCCCCTT TGTCTGATT TAAGCAGTGT GTACTTGGCA TCTCTACATT GTCCTAGGGA 720
 CAGTGGTGTT CTACAATATT ATCATGTATG ATGTTTATTT GGTGCTTTTT ATTCATAGTG 780
 50 GCTTCTTACC AGAAACAGTA GGAAGAAACA CATGAACTGT GTACAAGACA TGAAACATTG 840
 CTGCTGATAT GTGTTTTTTT CACATGCTTT TGAGTTTCA CTTTTTAAAC GAGAGCCAGC 900
 55 AAGCAAATA GATGTGGCTG GGTCTGCCTG TCCGGGCGGC TYTTTGCACC GAGCTCTCAA 960
 ATCCTGTGTA TTGAGGGTTC CTTTTTGGTA CTCAGGATTG GAGCTACAGC TGGGCCCCC 1020
 TCTCTCCCAT TCGTTTGAAG AGACACTGAG GGAAACAAGG GTTCTTTTTG AGGTGTCTTT 1080
 60

GGCTGCCTTT TACGGGATGG GAGCCTTCTC CGGATCTTTT GTTCTTCTGC ACCTCTTGTA 1140
 GCTACTGCCG GTGCAAGGTT GTAGATGTTA TTCCCCAGGA GCCTGGGCTK GGGGGCTGAG 1200
 5 CTGGGCTGAA TGCAAAAGCA TGCAACCAGA AGGCGGGCAA GGGGAGGAAA AGCAGGCCTG 1260
 GCCTCATTTG TCCCCTGGAG ATGTCTGTAG CAGTCAGCTC CAGCTTGGGC CTGGGGAAGC 1320
 AGCCTGACCA AGGCGCTCAG GTGTGCCTGT TACAAGAAGA ACCTGCAGAA GGATAATTTG 1380
 10 CACATGGAGC TGTGATAACA CTAATGTTGA TTTMTTTTIT TTTTACAAGT CATCAGRGAT 1440
 GTTTCGAAAG TGAGTTTAT TTTTGTGTA TTCTTTATC TTTACTTAAA GGTGAATGTG 1500
 15 TATTCCTCTG GGAGGAATAG GAAGAAAACA GGAATGTAA TAATGTCGAA CAGAAAACCT 1560
 CCTCCCTTAT TAATATATAA TCYTCATGTA TTTATGCCNT AATGTAAGCT GACTTTTAAA 1620
 AAGCTTTCTT TTGTTGCATG CCTGTGCAG GCATCTGTAT TGTACATGCA TGCCTTTCTG 1680
 20 CCTGTTTTCC TGTATAAAGT TAGTGAACAA AGAAATATTT TTGCCCTAGT TCATGTTGCC 1740
 AAGCAATGCA TATTTTTTAA ATTTGTCATA TATGGAAAGA GCATGTTGT TACATGTAAA 1800
 25 AGCTTTACTG ATATACAGAT AACTAATGT TTGAAGATGC TGTCTTTGC AAGTGTACAG 1860
 TTTTCAAATG TTGTTACCAG TGAAACACCC TTGTGGTTTA AACTTGCTAC AATGTATTTA 1920
 TTATTCATTT CCTCCCATGT AACTAAGAAT CATGGCTATA TTTTCATATCA ACGTTATATT 1980
 30 GAAAGTGAAG GGAAATGATT AATACAAGGT TTTGTAACAA AAAAAANAA ANNAAA 2036

35

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

45

GGCACGAGAT AACATAGGCA CAATAATACT GTATGTCTAC TTCTAGGATT ATAAGGAATT 60

AACATTGAGA TGACATTTCC ATTTGAGAAG AAAATAGTTG CTTTCAGTGC CTTTATTTG 120

50

ATTCTCTGGAG AGAGCAGACT CGCACCAACA TTCAACCCCA GCGCTGATAT GACAGTAATC 180

CTCAGAGGCA GAGCCCAGCA CAAAACAGCA ATGCTAGAAA GTTACAATTG GAAAGTTTCC 240

55

TGCCAGCTTC GGAATGACA CTGCAAAGCT GATGCCAGAA ACTGCCAGAG TAATTCTCCT 300

CATTACTGCT CTACCCACCC ACTTTCAGCT CCCCAAATTA ACTAGTGCAG TTGACTAATC 360

CTCTTTACCT TTATCATTTA GGTGAGGCAT TGCACAAAAA CTCTCGACTT TGCCATATAA 420

60

GGGCTGTGGT TCTCTGTGGT CCTGGATAAG AGGCATCACC ATTATCTGGA AACATGCAGT 480

5
 10
 AAATGCAGAT TCTTCATCTT CTCCCCAGAC CTCCTGAGTT AGAAATTCAC AAGTTCTCCA 540
 GGTGATCTCA TACATGCTAA AGTTTGAGAA CCATTGAGTA AAGTTAATGC ATTAAGAAGA 600
 GATTAGATAG GGATGGTGGC GTATCTTCCT ACAGTTTCCC TGTTAACAAG AAAGTCAGAG 660
 GTCAGTTGAT CAGACATTAG ATTATTTATT GCTAAACTA AAAAAAATTA AAAAAA 717

(2) INFORMATION FOR SEQ ID NO: 28:

15
 20
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

25
 30
 35
 40
 GAATTCGGCA CGAGCAGCAT CCTAATTTTA GTTTGGAGAT GCATTCTAAA GGATCTTCTC 60
 TATTGCTTTT TCTCCACAA TTAATCTTGA TTCTGCCTGT CTGTGCACAT TTGCATGAGG 120
 AACTGAACTG TTGTTTTCAT AGGTAAATGA GAGACTGAGT TTTTTCATTT CTGAAGAGAA 180
 AGGGCATTTG CTCCTACAAG CTGAAAGGCA CCCCTGGGTG GCTGGGGCCC TCGTGGGAGT 240
 TTCTGGGGGA TTGACCCCTA CAACATGCAG TGGCCCTACA GAAAAACCTG CAACTAAAAA 300
 TTATTTTFTA AAAAGGCTCC TCCAGGAAAT GCATATAAGG GCTAATCACC CAGTATTTTG 360
 ARGCTTCGAA GARGTAATAR AMCCCTGGAG AGAGAACTG AGACATGTAA GAGGGTGGGA 420
 ATGACTCAGT GGTGGCACAC TATGGAGTCC TGCCCAACAAG TAGCACACAT CAACCCACTA 480
 CACAGAAATC CTAGG 495

(2) INFORMATION FOR SEQ ID NO: 29:

45
 50
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

55
 60
 AGCTTAACGT CATGATTCAT TAGGGGAATG CAAGGCAAAA CCATGATGAG AATGCCCTA 60
 GACACCTCTT AGAAGAGCTG CTAGAAAGGC AGACAGCACC AAGCGCTTAA ATGAGATGGG 120
 GGCACCTGGT CTTCCTCTGT GCCTACTGGT AGGGGTGCAG CAGAGTGGTT CAGTCTGGGA 180
 CAGTTAGCTG GACATCACGT GGACCAACA CACGCATTTC CTGGGTACT TACCAAGGAG 240

AATAGAAAGC AGGCAGATCT TTACAGCAGC TCTTACCTGW TTGCAAAACA ATGGAAATGC 300
 CCACATGTCC ACAAACAAGT KTGTGGTCTG CCTGTGCCAT GAAGCACAGT GTGGCTGAGC 360
 5 GTCAAGAGTC CCCACACTCA AAGGAGGCAG CAGATACAGG GCTGCACACT GTGTGATTCC 420
 ACACATGTGA CATTTCTGGAC ACGGACATGC TGGATGGCAA AACGAGCATC GGGCTGAGAG 480
 10 GACTGCTGAG AAGGGGAACG GGGCTGCTGG GATGTGGGTT GATTGTAGCA GTAGCTCATG 540
 GAGATGTGAC CTCAA 556

15

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTAAATGGTG ACTGTGGCTT TGTGAGACA GGCCCCAAAT GGTAGGTGTG AACACAACAT 60
 GCACAGAATG AGGAGACATG CAGAGTGCTG AAATACTGTC CTGGACAGAT GTGTTACATG 120
 30 ACTTCTTTT CAGCTTATTT CTGTGGCCTG CCTTTGAAGA TAGAGCTTTG TTGATATTTA 180
 CATTAACCA AATTGTATAA YTATGTTCCA TTCTGACATG TTATTTAGCA AARGAAAAAR 240
 35 GAGTAATTCT ACATCAGCAT CTTTAGTGCA TGCTAAAAGA TTAAAAATGT CTTTGGGGA 300
 ACATGTTTTG TATACATAAA TGTTAGATA GAAATATTTA TAGAATNCTC TATGTGAGTA 360
 TTATCTCCC TATGTATATT TATATCTAGA TGTGTCAATC TTTGTATTGA TATGAAATGC 420
 40 TATGAATAGT GAGA 434

45

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCACGCTCC GATCTCACAG CTCGACACT ATGCGAGCC ATACACAACC TGGTGTGAGG 60
 AAACGTACTC CCAAATAAG CCAAGATGC AAAGTTTGGT TCAATGGGGG TTAGACAGCT 120
 60 ATGACTATCT CCAAAATGCA CTTCTGGAT TTTTCCGAG ACTTGGTGTT ATTGGTTTTG 180

CTGGCCTTAT TGGACTCCTT TTGGCTAGAG GTTCAAAAAT AAAGAAGCTA GTGTATCCGC 240
CTGGTTTCAT GGGATTAGCT GCCTCCCTCT ATTATCCACA ACAAGCCATC GTGTTTGCCC 300
5 AGGTCAGTGG GGAGAGATTA TATGACTGGG GTTTACGAGG ATATATAGTC ATAGAAGATT 360
TGTGGAAGGA GAACTTTCAA AAGCCAAGAA ATGTGAAGAA TTCACCTGGA ACTAAGTAGA 420
10 AAACTCCATG CTCTGCCATC TTAATCAGTT ATAGGTAAAC ATTGGAAC TCATAGAATA 480
ATCAGTATTT CTACAGAAAA ATGGCATAGA AGTCAGTATT GAATGTATTA AATTGGCTTT 540
CTTCTTCAGG AAAA ACTAGA CCAGACCTCT GTTATCTTCT GTGAAATCAT CCTACAAGCA 600
15 AACTAACCTG GAATCCCTTC ACCTAGAGAT AATGTACAAG CCTTAGAACT CCTCATTCTC 660
ATGTTGCTAT TTATGTACCT AATTAAAACC CAAGTTAAAA AAAAAAAAAA AAAAA 715
20

(2) INFORMATION FOR SEQ ID NO: 32:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GAGCCAGTGC CGGCGAAAGG GGACCTTCCT CTA CTTCCTG CCACAGACCC TGTCCCCACA 60
35 CACTTCCTGC CCCTGCTCTG CTGGGAGGCC ACTTCCTCCC CCAGTGCTGG ATTCCACCCC 120
CAGCTCACCC TCAAACATGG CCCCTCTCT CTCTCTGCTT GCCCCTCTCT GCTCCCTGGA 180
40 GGCTGTTCTG TCCTCCCCTC TTGAAAAGCA ATGCCAGCTT CCTGGGATCT TCTGCCAACT 240
CCAGCTACCA TGCCCTTTGC TCCTGTCAGC TCAGCTCCTC AAGGGAATTG TCTAMCCTCG 300
GTGTCTGCT TCCTCCCTC AACCTCCTCA CCTGTCTCCA AGCTGGCATC TGCCCTCCA 360
45 CTGCACAGAA CGGNTCCCC ACCACCTGCC TTTACAGGA GGAAGCAGCA ACATGGAAGA 420
ANCGAACTAT AGGGGCTACA ANGATGCTCA GCTCTGATCC CGAAGGCAAA AAGNATCTTT 480
GGGCAC 486
50

(2) INFORMATION FOR SEQ ID NO: 33:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 725 base pairs
(B) TYPE: nucleic acid
60 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

5 GTTCCTCTGG TAATAATTAG GTTATTCCCA GAAGCACAGT GTCATTCTTT AAATAAAAGC 60
 TTTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA AGATTCCCCC TAGGGTTGAT 120
 ATGTGTCTAA TTCATTTTAT AAAAATTATT CTGTCTTCA TTTTAAAGCT TTGGCTATAT 180
 10 AGTCAGAAAT GTCCTAAATA ACAAATATT TGTATTTAA TTTAGGAAG ACTAAAGGA 240
 AGAAAAATGA AAACCTCAGTC TTTATGTAAG CTCCAAGGAT ATTAGGGCTT AAAGGGCTTT 300
 15 TCTAGTTTGA TGAGAATTG TACTACTGAT TTTTATATAT TCCTGTTTTT GATGAACAGA 360
 TCTCTGGGGA AATTGTTGAG TTACAATGGC ATTTCACTGT GATCCCTCTC AAGCTCAGAT 420
 CAGTTCTATA ACCCAATGAC AACCTGTCTC TTTGGTTTAC TGTCCTGTGA AATGTCAGCT 480
 20 CAAGTTTCCC AGAAGTCGTG TGTATTATGAT GAGTCAGAGT GCTTTTCCTC GGTGGGACAG 540
 TTGCTGGCCC TCTTAATTTT GGTGTATGTG CTCCAAGTA TCTAAACCTC CAGTCTGATC 600
 TGTATATGCT ATCCTAACTG TTAATTGTAT TATTGATTAT GTTGATTATC TTGCTTGAAG 660
 25 GTTCATACTT TTCAATTGA TAGAAATAAA GTTTTTTCT GCTTATAAAA AAAAAAAAAA 720
 AAAAA 725
 30

(2) INFORMATION FOR SEQ ID NO: 34:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CACACAGCAT GCTGCCCTCA GACGTGTCCA TCCTGTACCA CATGAAAACG CTGCTGCTCC 60
 45 TGCAAGATAC TGAGAGATTG AAGCATGCTC TGGAAATGTT CCCAGAACAT TGCACGATGC 120
 CTCCTGCTTT TATTGGCTCT TGTGAAATC AAATTGGAAG ATCTTCAGTC CCAGCTGCAC 180
 CCAACGTGGA AAAGTATTC AGGTCCATCC CCAAGGAACC AACACCGATG ACATGGACTC 240
 50 AGGAATCTTA TAACCTACGT GGAATCTTTC CATCCGTACA TTGTCGTGCA CATGCCACTC 300
 ATCACCTGGC GTGCCAGAT CCTCGCARG CAACACCCTG TGATAATTCC AGGTGATTCT 360
 55 CTACATCTGC AGCTTGAGGT TAGCCTCATA TCACATTACA TTCTCACTAN AACNAAAAA 420
 AAAAAAAAAA AACTCNA 437

60

TTGGATCTTG GGAGTTTCT TTGTTTGCTC CTGTGTTTGC CCAGCTTTAA TAAAACCAGG 180
 CGCAAACAAA AACCATAGCA TTCTGAACAA TAGGGGGCCC ACATTGGACC CAGTATGTCA 240
 5 CTTTAATGGA CTTCAAGAAA AAATCTGAAT GGGAAAAATG AACTAGGAA TGTATACTCC 300
 ACACATTTTA TGCCATATAA TGGTGTGTTT TCTTAATTTT GTTCTTTGTG GCGAAATGTG 360
 10 GCTTTCAAAT TAAAATGACC TTTTCTTCTT TGAAACTTTT TGTTTTGACT TGTATAATTA 420
 AGGGTTTGA AAGATTCATA ATTCTGAGAG AGGTTTGCAA CCAGGAGATA CAAAGAAGTC 480
 TCAGTAGTAA TCTTGTTCAT GTGCTTTTAC AGCCAGCTAC ATTTAAGGAT GTATTAGTTA 540
 15 CAGAAATTAT ATGTCTGTGT ATGTGTCTCT ACTCAATAAA GTACATGCCT CCACAAAAAA 600
 AAAA 604

20

(2) INFORMATION FOR SEQ ID NO: 37:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GTGAGTGCCC GGGAGCCCCG AGGCCCTGCC CCTAAGAAGG ATATCTYTRA CCGCTCCCTT 60
 35 GTCCACACCC TAACCCCCCA GCTGCTCAGG CAGTGGGCAC ATGGCAGGGG CCTCACTGGG 120
 GGCACATAGA GCATTTGGGG GACTGCGAGT GCTCACCTTT GACTTCCTGC AGGTCGGGGG 180
 AAAACCAGAT CATGATGACC AAAGTYTACA TATTCTTGAT CTTTCATGGT CTGATCCTGC 240
 40 CCTCCCTGGG TCTCACCAGG TATATGCCAC CACYTCTGY TCTAAATCA GAATAAGAGT 300
 CACATCAGGA GAGCACTGTC CCCAGGANAA TGCAAACGGG TTGGCAGCA 349

45

(2) INFORMATION FOR SEQ ID NO: 38:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GTAGTCGTTG CGGTTGCCCG GATGGCGAAG ATCTCGCCGT TTGAAGTCGT AAAACGCACC 60
 60 TCGGTACCGG TGCTTGTGG TTTGGTGATT GTWATCGTTG CTACAGAGCT GATGGTGCCA 120

GGAACGGCAG CAGCGGTCAC AGGCAAGTAA ATAGTAATGC CGGAGCAAGT TTCCTCCGGC 180
 TTTATCATGT CACCCACTGT GGTATATGCG TTGTGGTCTG CCAACTTTGC CGTGAACAAT 240
 5 TTCAGCAATA ATCAGATGGC GGCTGGCGCA ATATTCAAGA TAACGCCTGG CAGTGGTGCG 300
 GCTGATGGTT CAGTGCCTGC GSCACCGTTT YTCCCGTATG TTGCACACCA GGNICTTTAA 360
 10 ACAGTTTTCG SACCGCGTTT AGCGTCAAGG GTTCAATGCC GGTCGGTAGC TCGTCCTTAG 420
 GTTCACCGCG AGCATAAGCA TTAAACATCT CATCAATTTC CTCTGGCTG GCGCTATCAA 480
 TACTTTCCAG CATATGTTTA CGCTGGCGGA AACGGGTAG CGTTTGCCCC ARCMGWTCAT 540
 15 AGGCAATGGG CTTAATGAGA TAATCAAATA CACCACAACG TACGGCTTCA GACACCGTTT 600
 CCATATCGCT GGCTGCAGTG GTAAACACCA CGTCGCCGGG ATAATGCGCC TGCACCAGTT 660
 CATGCAGTAA AT 672
 20

(2) INFORMATION FOR SEQ ID NO: 39:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AGAGTTGATA TTTTAGAAA CAGTAATTTT ACTTTTAAGG AAATTGGCTA GCTCTTTGAC 60
 35 TNNAGAGCTG TAGGAAGCTC AACATTTCTT TGTAGAGAAC GTTGCTTTTT TTGGATTGTA 120
 CAGGTATAAA AACATTGCTT TTGTTGAATT GTATAGGTGT AAAAAGGGAA TAACTGTATG 180
 40 CAGGTTTGAA AAGGAAATGT GCTTTAGGCA TGAGTCATAA GATGCCATTG TACTTGTAGG 240
 CATTTTATTT TCCTTTAGAA ATGGACATCA GCTCTTCTCT TCTGACTGGT AACACATAGC 300
 45 CCCAAAGCAT GAGATTATTT TTCATTGGGT TTTTATGTT GTTTAGTTTT GGTTTGTTAC 360
 GCCAGCCCAG TCTGTCTGCG GAACACTGAC TCTGCTCTCT AATGAGAACA AAGTTAGAAA 420
 TCTGCCGATA ACCTAAAATA ATTTAGAAAT GAATTAAGAA TGTGAAATCG GGTAAAGTG 480
 50 ATGATGATAA AATAGCATGC AAGAAACAAG CTCCTTCCAT CAGACTTGGC TACTGTTTTTC 540
 TTCTGGTACG ATTTGGTTTG GAAGAGCCTC TTGTTTCCTT CTCTTTGGGG TATGTCCTCG 600
 TTTCTTAATA TGTMTGTAAC ATTATTGAGA TATAATTCAC ATACCTTACA ATTCACTTAT 660
 55 TTTAAGGGTA CAATTTAGTG GTTTTAGTG TATTCACAAA GTTGTGTAAC CGTGACCACA 720
 GTCAATTTTA GAACATTTTC TTACCCCAA AAGAAACCCT GTACCCTTGA GCAGTCACCT 780
 60 CTCATTTTCT CCCAGTGCCC ACCCCATCCC CGAGCCCKG GAACCACTAA TCTATTTCTC 840

TCTCTGTAGA TTGCTTATT CTGGTCATTT CATATAAATG GAATCTTACA ATATTCGGTC 900
 5 TTTTGGGACT GGCTTCCCAA ATATGATTTT CTATATGGAG TGAGAAAATT CTTCTCATCT 960
 TGAGAACTCT TATTGCTGTG AAAGGGAGTG GTTGGTAAAA TCAATAGATT TCAGGCAAGA 1020
 GGGCCAGATA CCTAACAGGT TTTCTCCGT GAATCTTATG CTGAGTAGTT TTTCTCATA 1080
 10 ACCAAGCATT TATGATATAT TACTACTTAT AATACTGTGG CTAGTCTCTA GAATGGATGT 1140
 TGAAATCTTT GCCTCCTCAG TCGGAAGAG TCCTGCTAAA AATCAGGCTA AAAATCAGGC 1200
 CAAAAATCAG GCCAAATGAC TTGGCAAATA ATTGACAAAG TGGTTTTTAC GTGTGTCTAT 1260
 15 CTTTGCTAGC AGCTTGATA CCTCAGGCCA GGTGAGCTCC CCAAATTTCT TTTTTCATTT 1320
 ACTCCAGTGA GTTCTGCTG TCTTTTCAA GTATGTACCA TAGGACTTAA AGGTGATTG 1380
 20 GATGCGTTGT AACACTGCTA AATATGCTAA GTACAGAATT TTATCTACAG TACTGTGAGA 1440
 CAGTCAATTA TTGCCTAGG TAGTTCAAAA ATATGATGTG AGCTAGTTAA GCCTTTGCTT 1500
 GACTGATTTT AGTGATATTC AGAAGTGTGT ACCAATCAAG GCTCTTTAAA ATACGGAACG 1560
 25 ACTCACTTAA TAACCAGGGA ACCAGCCAAA TACTGTGCAG CCGCAGAATA TGCATATCAA 1620
 TGAGTTGGAG GTGATTATTC TCTGTAATC CCTAATGATT GTTTTCTAAG CATTGTGGCT 1680
 30 TCTCAGTGGC TTGACAGCAT CTCTCTGGT GTATGTGGCC TGTTTACATG ATGTATTGAA 1740
 TAATGTTGTT TGTGTGAGC ATCAATGCCT GTAACACCAA ACTAAACACG TGTTTTTGGG 1800
 ATATGTTTCC AATCTTTAAA TGACCTTGCC CTGTCCAATA AATAAATGAT TGTCTCACC 1860
 35 TGTAAAAAA AAAAAAATT AAAAAACTG GNGGGGGGC CCGGTACN 1908

40

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CCTCAAAAAA AAAAANGAAA GGAAAGAGGT CTCTACACAA GCCCGTGATT CTTCATGGCA 60
 AGGGATAACA TCAGAAATGT TTCATTTYCK GCTATTAGTT TCCATTCCCTT TCCCCATCCA 120
 55 GGCATAAAGA GAAACAAAAG ACAATGATGG TATTCTCTGT GTCCTCAGCT TTGGCACTTT 180
 TGTGTGATGT GCTAAGGAGC AGTGACCTTG CTAAAAAGAC TGAATAATCC ACCCACTGAA 240
 60 TAGCTAACCT GGGGAGGAAA TGAAAATTTT CTTTGTGGAT CTCCCCAAAT CCATTGTTGT 300

CACCAGGCCC TCCCAGAACC TCCTCAGTTC CTTACAGTG CAACCTGTG TACTTGCCCC 360
 GCAACCCAAT AGTATGTGTC CTCACTTCAC CTTCCATGGG CAACTGCCCT CCCTTCTGGA 420
 5 CATAAAACCT CATATTTTAA ATNAAGTTGA AATTGAA 458

10 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1153 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

20 GGCACAGAGC CTCGACCCA GGTGGTCTGG AGCCTGCCGG GAGAGTGGTG GCATCTGAGA 60
 GGCTGGTCGT GGACTGTGGT TGGGGGAGGT GGGAGCTGTT TTAACCGTGT GCCCCTCTC 120
 CTGTGCCGGC GTGGGCATCC CCCGGGCGAG TGAACCCGG GCGCTCCTCC AGCTTCCGAG 180
 25 TCCAGCCAGC CTGGGCGCGG GGCGCGCCCC GAGACACCCG AGGAGTCCGT TCCTCCCTGG 240
 TTACGTGGAC TGTGGAGCTG GTCTCTGTG GCTCAGCGCC GTGCGGAGGT TGAAGCGTAC 300
 30 CTGCGGAGGT CGCACCAGG CGTGAGGAGG ACGAGGAAG GCATGAGCCG AGCTTGAGGA 360
 ATCCGTGCTC CAAACTCTAC ACTCAAGGAT GCACTGCGCA ACTCTGGTGG CGATGGGCTG 420
 GGCAGATGT CTTTGGAGTT CTACCAGAAG AAGAAGTCTC GCTGGCCATT CTCAGACGAG 480
 35 TGCATCCCAT GGAAGTGTG GACGGTCAAG GTGCATGTGG TAGCCCTGGC CACGGAGCAG 540
 GAGCGGCAGA TCTGCCGGA GAAGGTGGGT GAGAACTCT GCGAGAAGAT CATCAACATC 600
 40 GTGGAGGTGA TGAATCGCA TGAGTACTTG CCCAAGATGC CCACACAGTC GGAGGTGGAT 660
 AACGTGTTTG ACACAGGCTT GCGGGACGTG CAGCCCTACC TGTACAAGAT CTCCTTCCAG 720
 ATCACTGATG CCCTGGGCAC CTCAGTCACC ACCACCATGC GCAGGCTCAT CAAAGACACC 780
 45 CTGCCCTCTG ACGCTCGCTG GATCTCTGGG AGCTCCTTGA TGGCTCCAG ACCTTGGCTT 840
 TTGGGAATTG CACTTTTGGG CCTTTGGGCT CTGGAACCTG CTCTGGGTCA TTGGTGAGAC 900
 50 TTGAAGGGG CAGCCCCCGC TGGCTTCTTG GTTTTGTGGT TGCCAGCCTC AGGTCATCCT 960
 TTAAATCTTT GCTGACGGTT CAGTCCTGCC TCTACTGTCT CTCCATAGCC CTGGTGGGT 1020
 CCCCCTCTT TCTCCACTGT ACAGAAGAGC CACCACTGGG ATGGGGAATA AAGTTGAGAA 1080
 55 CATGAGTTTG GGCTGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
 AAAAAAAAAA AAA 1153

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(2) INFORMATION FOR SEQ ID NO: 42:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1983 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

	GGCACGAGAG GGGCCGAGCC GACAAGATGT TCTTGCTGCC TCTTCCGGCT GCGGGGCGAG	60
15	TAGTCGTCCG ACGTCTGGCC GTGAGACGTT TCGGGAGCCG GAGTCTCTCC ACCGCAGACA	120
	TGACGAAGGG CCTTGTTTGA GGAATCTATT CCAAAGAAAA AGAAGATGAT GTGCCACAGT	180
	TCACAAGTGC AGGAGAGAAT TTTGATAAAT TGTTAGCTGG AAAGCTGAGA GAGACTTTGA	240
20	ACATATCTGG ACCACCTCTG AAGGCAGGGA AGACTCGAAC CTTTATGTTT CTGCATCAGG	300
	ACTTCCCCAG CGTGGTGCTA GTTGGCCTCG GCAAAAAGGC AGCTGGAATC GACGAACAGG	360
25	AAAACGGCA TGAAGCAAAA GAAAACATCA GAGCTGCTGT TGCAGCGGGG TGCAGGCAGA	420
	TTCAAGACCT GGAGCTCTCG TCTGTGGARG TGGATCCCTG TGGAGACGCT CAGGCTGCTG	480
	CGGAGGGAGC GGTGCTTGGT CTCTATGAAT ACGATGACCT AAAGCAAAAA AAGAAGATGG	540
30	CTGTGTCCGG AAAGCTCTAT GGAAGTGGGG ATCAGGAGGC CTGGCAGAAA GGAGTCTCTG	600
	TGTCTTCTGG GCAGAACTTG GCACGCCAAT TGATGGAGAC GCCAGCCAAT GAGATGACGC	660
35	CAACCAGATT TGCCGAAATT ATTGAGAAGA ATCTCAAAAG TGCTAGTAGT AAAACCGAGG	720
	TCCATATCAG ACCCAAGTCT TGGATTGAGG AACAGGCAAT GGGATCATTC CTCAGTGTGG	780
	CCAAAGGATC TGACGAGCCC CCAGTCTTCT TGGAAATTCA CTACAAAGGC AGCCCCAATG	840
40	CAAACGAACC ACCCTGGTG TTTGTTGGGA AAGGAATTAC CTTTGACAGT GGTGGTATCT	900
	CCATCAAGGC TTCTGCAAAT ATGGACCTCA TGAGGGCTGA CATGGGAGGA GCTGCAACTA	960
45	TATGCTCAGC CATCGTGTCT GCTGCAAAGC TTAATTTGCC CATTAATATT ATAGGTCTGG	1020
	CCCCTCTTTG TGAAAATATG CCCAGCGGCA AGGCCAACAA GCCGGGGGAT GTTGTTAGAG	1080
	CCAAAAACGG GAAGACCATC CAGGTTGATA AACTGATGC TGAGGGGAGG CTCATACTGG	1140
50	CTGATGCGCT CTGTTACGCA CACACGTTTA ACCCGAAGNT CATCTCAAT GCCGCCACCT	1200
	TAACAGGTGC CATGGATGTA GCTTTGGGAT CAGGTGCCAC TGGGTCTTTT ACCAATTCAT	1260
55	CCTGGCTCTG GAACAACTC TTCGAGGCCA GCATTGAAAC AGGGGACCGT GTCTGGAGGA	1320
	TGCCTCTCTT CGAACATTAT ACAAGACAGG TTGTAGATTG CCAGCTTGCT GATGTTAACA	1380
60	ACATTGGAAG ATACAGATCT GCAGGAGCAT GTACAGCTGC AGCATTCTCG AAAGAATTGG	1440

TAACTCATCC TAAGTGGGCA CATTTAGACA TAGCAGGCGT GATGACCAAC AAAGATGAAG 1500
 TTCCCTATCT ACGGAAAGGC ATGACTGGGA GGCCCAACAG GACTCTCATT GAGTTCCTAC 1560
 5 TTCGTTTCAG TCAAGACAAT GCTTAGTTCA GATACTCAAA AATGTCTTCA CTCTGCTTTA 1620
 AATTGGACAG TTGAACCTAA AAGGTTTTTG AATAAATGGA TGAAAATCTT TTAACGGAGA 1680
 10 CAAAGGATGG TATTTAAAAA TGTAGAACAC AATGAAATTT GTATGCCTTG ATTTTTTTTT 1740
 CATTTACAC AAAGATTTAT AAAGGTAAAG TTAATATCTT ACTTGATAAG GATTTTTAAG 1800
 ATACTCTATA AATGATTAAA ATTTTATAGAA CTTCCTAATC ACTTTTCAGA GTATATGTTT 1860
 15 TTCATTGAGA AGCAAAATG TAACTCAGAT TTGTGATGCT AGGAACATGA GCAAACTGAA 1920
 AATTACTATG CACTTGTCAG AAACAATAAA TGCAACTTGT TGTGCAAAAA AAAAAAAAAA 1980
 AAA 1983
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25 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1406 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGATGATGA CTTTGAAGAC GATTTTATTC CTCTTCCTCC AGCTAAGCGC CTTGAGGTTA 60
 35 ATAGTTGGAA AAGACTCTAT AGATATTGAC ATTTCTTCAA GGAGAAGAGA AGATCAGTCT 120
 TTAAGGCTTA ATGCCTAAGC NCTTGGTCTT AACTTGACCT GGGATAACTA CTTTAAAGAA 180
 40 ATAAAAAATT CCAGTCAATT ATTCCTCAAC TGAAAGTTTA GTGGCAGCAC TTCTATTGTC 240
 CCTTCACCTA TCAGCATACT ATTGTAGAAA GTGTACAGCA TACTGACTCA ATTCTTAAGT 300
 CTGATTTGTG CAAATTTTTA TCGTACTTTT TAAATAGCCT TCTTACGTGC AATTCTGAGT 360
 45 TAGAGGTAAA GCCCTGTTGT AAAATAAAGG CTCAAGCAAA ATTGTACAGT GATAGCAACT 420
 TTCCACACAG GACGTTGAAA ACAGTAATGT GGCTACACAG TTTTTTTAAC TGTAAGAGCA 480
 50 TCAGCTGGCT CTTTAATATA TGAATAAACA ATAATTTAAA ACAAATCATA GTAGCAGCAT 540
 ATTAAGGGTT TCTAGTATGC TAATATCACC AGCAATGATC TTTGGCTTTT TGATTTATTT 600
 GCTAGATGTT TCCCCCTTGG AGTTTGTGCA GTTTCACACT GTTTGCTGGC CCAGGTGTAC 660
 55 TGTGTTGGC CTTTGTAAAT ATCGCAAACC ATTGGTTGGG AGTCAGATG GTTCTTTAAA 720
 AAAAAAAAAA AAAACGACAT ACGTGACAGC TCACTTTTCA GTTCATTATA TGTACCGAGG 780
 60 GTAGCAGTGT GTGGGATGAG GTTCGATACA GNCGTATTTA TTGCTTGTC TGTAAATTAA 840

AAACCTTGTA TTAACTCTT TTCAATCCTT TTAGATAAAA TTGTTCTTTG CAAGAATGAT 900
 TGGTGCTTAT TTTTCAAAA ATTTGCTGTG AACACGTGA TGACAACAAG CAACATTTAT 960
 5 CTAATGAAGT ACAGCTATCT TAATTTGGTT CTCAAGTTT TCTGKTGCAC TTGTAAAATG 1020
 CTACAAGGAA TATTAAAAA ATCTATTCAC TTAACTTAT AATAGTTTAT GAAATAAAAA 1080
 10 CATGAGTCAC AGCTTTTGTT CTGTGGTAAC CTATAAAAA AGTTTGTCTT TGAGATTCAA 1140
 TGTAAGAAGC TGAACAACAT GTATATGTTG TAAATATTG TGTTTGTGA GAAATTTTGT 1200
 TCATAAGAAA TTAAGAAGC TTACCAGGAA GGTTTTAAAG TTAGAAATAT TCCATGCCAA 1260
 15 TAAATAGGA AATTATAAAT ATATAGTTT AAGCCTGCAT CAGTGGGAGT CTGGGCTATG 1320
 TAGTTATGTA GTTATTATGN AACCACCAAG ATTTTGTGG CTATTTACCG TAACCAAAGG 1380
 20 GGCCGATTAA NTGGTTTGAA GNCTTG 1406

25 (2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1391 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

35 GGGCCTGAAG GCGGCRGCC AGTCCCAGC AGTGCTCGCT CCTGCTCGGG GCGCTGCGG 60
 CCCGGGCGTC GCCATGACCA GTGAGCTGGA CATCTTCGTG GGAACACGA CCCTTATCGA 120
 CGAGGACGTG TATCGCCTCT GGCTCGATGG TTAAGCTGGT ACCGACGCGG TGGCCCTGCG 180
 40 GGTGCGCTCG GGAATCCTGG AGCAGACTGG CGCCACGGCA GCGGTGCTGC AGAGCGACAC 240
 CATGGACCAT TACCGCACCT TCCACATGCT CGAGCGGCTG CTGCATGCGC CGCCAAGCT 300
 45 ACTGCACCAG CTCATCTTCC AGATTCCGCC CTCCCGGCAG GCACTACTCA TCGAGAGGTA 360
 CTATGCCTTT GATGAGGCTT TTGTTGCGGA GGTGCTGGGC AAGAAGCTGT CCAAAGGCAC 420
 CAAGAAAGAC CTGGATGACA TCAGACCAA AACAGGCATC ACCCTCAAGA GCTGCCGGAG 480
 50 ACAGTTTGAC AACTTTAAAC GGGTCTTCAA GGTGGTAGAG GAAATGCGGG GCTCCCTGCT 540
 GGACAATATT CAGCAACACT TCCTCCTCTC TGACCGGTTG GCCAGGGACT ATGCAGCCAT 600
 55 CGTCTTCTTT GCTAACAACC GCTTTGAGAC AGGGAAGAAA AACTGCAGT ATCTGAGCTT 660
 CGGTGACTTT GCCTCTGCG CTGAGCTCAT GATCCAAAAC TGGACCCTTG GACCCGTCGA 720
 CTCACAGATG GATGACATGG ACATGGACTT AGACAGGAAT TTCTCCAGGA CTGAAGGAG 780
 60

CTCAAGGTGC TAGTGGCTGA CAAGGACCTT CTGGACCTGC ACAAGAGCCT GGTGTGCACT 840
GCTCTCCGGG AAAGCTGGGC GTCTTCTCTG AGATGGAAGC CAACTTCAAG AACCTGTCCC 900
5 GGGGGCTGGT GAACGTGCCG CCAAGCTGAC CCACAATAAA GATGTCAGAG ACCTGTTTGT 960
GGACCTCGTG GAGAAGTTTG TGAACCCCTG CCGCTCCGAC CACTGGCCAC TCAGCGACGT 1020
GCGGTTCCTC CTGAATCAGT ATTCAGCGTC TGTCCAATCC CTCGATGGCT TCCGACACCA 1080
10 GGCCCTCTGG GACCGCTACA TGGGCACCCT CCGGGCTGC CTCTGCGCC TGTATCATGA 1140
CTGAGGTGCC TCCCAACGTC CGCCACGCT GACAATAAAG TTGCTCTGAG TTTGGAGACT 1200
15 GGTCTCTGCT CCGGGGAGCA AGTGGGGGGC GTGCAGATGT GCCTGTGTCT GTCTCTGAGC 1260
ACCTGGTGTC CGTGTACAAG GATGGATGTG TNCNGTGGCT CCTTGGGAAC TGAGACATAT 1320
CTCAGGGAAT GGTGTCTGTG CTCAGCCCAT CCACCAGAAG AGTCTGCTCA CAAAAAAAAA 1380
20 AAAAAAAAAA A 1391

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(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1569 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GGCACGAGTG GAGATGGCTG CGGCCGTGGC GGGGATGCTG CGAGGGGGTC TCCTGCCCCA 60
GGCGGGCCCG CTGCCTACCC TCCAGACTGT CCGCTATGGC TCCAAGGCTG TTACCCGCCA 120
40 CCGTCGTGTG ATGCACCTTC AGCGGCAGAA GCTGATGGCT GTGACTGAAT ATATCCCCC 180
GAAACCAGCC ATCCACCCAT CATGCCTGCC ATCTCCTCCC AGCCCCCAC AGGAGGAGAT 240
AGGCCTCATC AGGCTTCTCC GCCGGGAGAT AGCAGCAGTT TTCCAGGACA ACCGAATGAT 300
45 AGCCGTCTGC CAGAATGTGG CTCTGAGTGC AGAGGACAAG CTTCTTATTG CGACACCAGC 360
TGCGGAAACA CAAGATCCTG ATGAAGGTCT TCCCCAACCA GGTCTGAAA GCCCTTCCTG 420
50 GAGGATTCCA AGTACCAAAA TCTGCTGCCC CTTTPTGTGG GGCACAACAT GCTGCTGGTC 480
AGTGAAGAGC CCAAGGTCAA GGAGATGGTA CGGATCTTAA GGGACTGTGC CATTCCTGCC 540
GCTGCTAGGT GGCTGCATIG ATGACACCAT CCTCAGCAGG CAGGGCTTTA TCAACTACTC 600
55 CAAGCTCCCC AGCCTGCCCC TGGTGAGGG GGAGCTTGTA GGAGGCCTCA CCTGCCTCAC 660
AGCCCAGACC CACTCCCTGC TCCAGCACCA GCCCCTCCAG CTGACCACCC TGTGAGACCA 720
60 GTACATCAGA GAGCAACGCG AGRAAGGATT CTGTCATGTC GGCCAATGGG AAGCCAGATC 780

CTGACACTGT TCCGGACTCG TAGCCAGCCT GTTtagccag CCCTGCGCAT AAATACACTC 840
 TCGGTATTG GCTGTGCTCT CCTCAATGGG ACATGTGGAA GAACTTGGGG TCGGGGAGTG 900
 5 TGTMTGTCAC TTGGTTTTCA CTAGTAATGA TATGTGTCAGG TATAGGGCCA CTTGGAGATG 960
 CAGAGGATTC CATTTAGAT GTCAGTCACC GGCTTCGTCC TTAGTTTTCC CAACTTGGGA 1020
 10 CGTGATAGGA GCAAAGTCTC TCCATTCTCC AGGTCCAAGG CAGAGATCCT GAAAAGATAG 1080
 GGCTATTGTC CCCTGCCTCC TTGGTCACTG CCTCTGCTG CACGGGCTCC TGAGCCCACT 1140
 CCCTTGGGGC ACAACCTGCC ACTGCCACAG TAGCTCAACC AAGCAGTTGT GCTGAGAATG 1200
 15 GCACCTGGTG AGAGCCTGCT GTGTGCCAGG CTTGTGCTG AGTGCTGTTA CATGTATTAG 1260
 TTCCTTTACT GCTGACCACA TTGTACCCAT TTCACAGAGA AGGAGCAGAG AAATTAAGTG 1320
 20 GCTTGCTCAA GGTCATGCAG TTAGTAAGTG GCAGAACAGG GACTTGAACC AAGCCCTCTG 1380
 CTCTGAAGAC CGCGTCCTGA ATTCTTCAC TAGAGCTTCC TCATCAGGTT ACCCAGAAGT 1440
 GGGTCCCATC CACCATCCAG GTGTGCTTGG ATGTTAGTTC TCCACCCTCG AGGTGTACGC 1500
 25 TGTGAAAAGT TTGGGAGCAC TGCTTTATAA TAAAATGAAA TATATTCTAA AAAAAAAAAA 1560
 AAAAAAAAAA 1569

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(2) INFORMATION FOR SEQ ID NO: 46:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1924 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGGCCCCCCC WCGWKTTTTT TTTTTTTTTT TTAAATTAGG ATAATGCCTT TATTAACGAG 60
 45 AATGAAACGT TCATTCTCTC TTCCACTCCT TCTCGTGGT TTTCTGGACA CAGCTCACCT 120
 GATCCTGCTA GAAACGTTGT CAGTCTGCTT GTGGCTTCCC TCCTTGATTG ACTCACGCTG 180
 TGTGATGTCT TGAGAAGTAT CTATCCACTT CATGTGAATG AGCACTCCAA TATCAGCCAA 240
 50 CATCAATCAT TCTTACCTAA AGAATAATAA GAAAAAGTTA ATATAAAAGA CAAGGTATA 300
 AAATAAAGGT TTGAAAATGC TAGTCAACTT CAAAATTAA AGAGTAAAAA TCCAGAGATA 360
 55 AAGATTGGGG GTAAGTTACA GCATAAAAAA ATAGGAAGAA ACTTCATGGT GGGGGGAAA 420
 TCTAAAATTA TTCTTACATA AAATAAGTAG ACACCTGAAT TAGAATGAAA ACTGTATTTT 480
 CTTTAAAATG TAAAAGCCTG ACTCTCAGTT TCACCAGTCT GAGCACAAGT TTGACTGCAA 540
 60

	CCCCAAATAT ACTATCCCTT ATGTGAAGGT ATGTGACAAC GTTGACCTCA CCAAATGAGT	600
	TTTAACATCA GCTCTTTTTT CATATGAAAG CACATACCCT GCTCCCCATT CAAGTATGTC	660
5	TTCCATTGTC AGGCAGGCTG ACCACCTTCA GCAGGAGTCC TCCAAGAGTG CCCAACTCCC	720
	CTTCCCACAG TACACAACGC TGTAGTTGTT GTCTTGCAAT CCTTTGTATT TACCTCATTC	780
10	TTTCCCATCT AAGTCCTCAC TGAGTTTAA AGTTAGGGCT GGAAAAGCTA TGCCTTACTG	840
	GGACAGCAAG GAACCAATTT TTTTCTGAGG GAGAAGACAT TCACCTTCAC TATATGCCCTG	900
	GCAGGGCCAC AGTGCACAAA ACAAAGATCA GCCTTCATTTC AAGTTCAGG TTTTCTTCC	960
15	TCCCTGAATG ATTACTGCAA AGGGTATATG AAGTAAGAGT TCCCTGTTGC ACATGTACCA	1020
	TCCATAAGGG ATACTATATC GTTTTGCAAT CTTCCCCCA TTCTCCACAT TGTCTATCT	1080
20	TAAGTCCAAG CCTTTTCAC TCTCAAAAAA AAAAAAAAAA TATTTTTTTC AGCACTGGTG	1140
	TTCAAAAGCA ACGTTTTTAT GGTAAATGGT TTACCAGCAA CTGTTGAGAT TTCCAGTTGA	1200
	GTCTTAAAAA TTGCCAATCA TTATCTAGCA GCAATGACAG ATGATTAGGA GCAGTCAAAT	1260
25	CCTCTGAATT CTTTCCCTAA TAGGCAGCCA TTTGAGAACT GCACTAGCTG ACATCACTAA	1320
	AACATTATCA GCTAAAGCCA AAACCAAATA AAGGCCAGA CCAACATCCT GGCTCTCTAA	1380
30	AACCTGTCCA AAATCATTAA GTGAAAGGCA GTAAATGCAG GACTGTGGAT CATGTCACTG	1440
	CAGCTGACAA TGATTAAACAA TAGGAGACAT GCAACCCCCA TTAAGGTTAA AAGTCCAAAA	1500
	CTAGTCACAC GCATCTCTTT ATTGGGAAA AGTGAGACTA TTATGCATTTC TTGGTAGGTT	1560
35	TGCAACCTTG CATGAAGAGC ACCCATTGCA TTTCTTTCAT CTTTCAGAAA GCACCGGTAT	1620
	CTGTTCCAAG GGCCTAACAG TACGAAAATA CATCTCTGCA TCACACCTCT GAACCCAAGA	1680
40	CTGTTCTCAT TAAAAATAAT TTTGGTTTGT AACAAAATTA TGAAATACAA TGCAAGCACC	1740
	TGGGTATAGC ATTATTACTG AAACCACTTA ATTCCCAGCT TTTTGAGTTT TTTAAAAAAA	1800
	CCCACTGCAC TAAGATTAC AATTCAATGC TACATACAAA TTAAAGCTAG TAAGAACACA	1860
45	CTAACGTCAC AAGTTTCTCA TTCTAAAGTG CAAAAGCCTA ATCATCTGAA AGTGAACAGG	1920
	GTAA	1924

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(2) INFORMATION FOR SEQ ID NO: 47:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

5 TGGTGTGGGG CCCAGAAAMC AAGGGACCAG TGAAAACAMC CCCAGAGACT TGTATCCGCC 60
 AGGAAAGCCA TTGCCAMTYC TGAGCCCTTG AAGGGCAAGG AGGGAAACAG TGTTACCAGA 120
 GCCCAGTAAG AACTGCTGTC ATGAAGGAGG GGCCACCTTG TAAGAGACAT CATTACTACC 180
 AGAACTGTGG TGCCAAATTG CTGGTGTCTC TCTTTGGAGA AACCAACCAG ATACATCTGC 240
 10 TGGAGACCCA GGTGGGCACA GAGAAGGGTG GAGAGAGAAT CTGGAAGAG AAATGGAGAA 300
 TAAGCAGCAC AGTGTATTTC ATTTCTGTAA ATTCTATGT AGAAGGCTCA GTGTTAGAAA 360
 TAAAGTTATT CTAAGTAGTTG CAAGTTAAGT GTTTCTGTTT GTTCTGCTTT CCTGTTAGCA 420
 15 TAAGTAAACT CCCTTTGGAA CTACACAGGT ATGTCTCTCC TTCAACATGT GTGAA 475

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(2) INFORMATION FOR SEQ ID NO: 48:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

AAGGGACAGA GACCTGGATT CAGATCTCAT TTTACAATGA AGACCCCAAT GCAGAAAGTC 60
 ATGTCTGAAA TTCTGAGCTT ACTCTCTGC CTGCTGGGAC CTGCTCTGGA TGAGAGAAGG 120
 35 GAGGAAAAGG ACTAATCAGA GGAGCCAATG AAGTCACTCC ATGAGTTTCC TGAACCCTGC 180
 CCAGCTAGAG ATTAACGTYT GACCTTCAAC GTAGGACACT GTGCAGATGG CTAAGTGTCTG 240
 GCGCACATGA AGACCAAAGC CAGGACCAAG CCCCMASCCT GCTWAACAG GCAGARTCTT 300
 40 GCCCAGCCMA CYTCTGTGAR AATCTGCTTC CCTCCACAGC TGACCC 346

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(2) INFORMATION FOR SEQ ID NO: 49:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TAGGTGTCAG CCGCCACCCC CCCCCCATAT GCAGATTAC TSGGCATGGT AGTGGCCAGC 60
 TTCTAACACA GCTGGTATTT CAAGTCTCCT GGGACCTCAC TCAGGAATGA TACCCCTCA 120
 60 GTAGAAGCAG CAGGTGATCT TAACTCCTTT CAAAGAGCAG GCCTGTCTGG GAAGCCATGT 180

	CCTCAGCAGG CACAGCAACC CCTCTGGAAA TGGATCACAA ACTCACTTCT CAGCCAGGCA	240
5	GGCCAAGCTT CTATTGTAAC AGTAGGCACA GTATAGTCGG ATCATCACAT CAGCTGGGTT	300
	TTTGGTTTAG TCATCTAGAG TCGTCTGGAC TAAAGGTCTT TCAGGTCTCC TTGCCCTGTG	360
	AGTGCGTGAA CCTCCCCACC CGAATTGCCT CAGTTGTCCT GAGCCTCATG TCTCTCCTGG	420
10	TGGTGGGCCA GGCCCTTGCA TGGGAAGGGA GCCTGCTGCG GGGCAGGCCA GCTGGGGGTG	480
	CTCACCTATG CGCAATGANA GTTATTGAAG GACTGGTTGT TGATGTTGGT GAGCGTATCC	540
15	TTCATGGCCA GCGCGAAGTC GGCCAGGTCA GCCAGGTGCT GCCAGCGCTC TCTCTCGGAC	600
	TTGTCTTCCT GTGCCAGGGG ACCGTGGAGA AAGTGTGAGG GGCCGCTCAC TGCAGCAGCC	660
	TGCTCTGCTG CCTTCCCTGG CAGTGTTCCT GGGGTGGATT CCTACAMCT AGATGTTCAA	720
20	GGCCTTACTT TTCTCTCCAC AAAGGAGTCG CAGCCACGCT AGCTCTGACT TGCCACTGTG	780
	ACAAAGTTCA CGTAGCAGGT CTAGGCAAAG ACTGGGCAAT TGAGCAGAGG AGACGGACCT	840
25	GTGAGTCTGA CCRYGAGSCG GRCCTTCA CCMGGCTGG GCTGGTCCTG GTCCTTAGGT	900
	TTTGTGAGGT TGTCTTGT TGGATCCCTC AACTAGGTGA TAAGCACTGG AGGGGGATGA	960
	CCCCCTTGG ACGTGTCTTCT TTAACCTCAT CCATATAATA GGGCCGTGGG ATGGTTGTAG	1020
30	AGGTAAAGCA GGATGATGCT GTTTAAGAC CAGAGCTTGG GACCAGGGCT CCTACACCTA	1080
	ATTTTCTCTC CTGGTAGCTG AACAAAGGTC TAAATTAGCT TAACAAAAGA ACAGGCTGCC	1140
35	GTCAGCCAGA GTTCTGAAGG CCATGCTTTC AGTTTCCCTT GTTGACAATT GCTCTCCAGT	1200
	TCCTATGAAA GCACAGAGCC TAGGGGGCC TGGCCACAGA ACACAACCAT CTTAGGCCTG	1260
	AGCTGTGAAC AGCAGGGGGT TGTGTGTCTG TTCTGTTTCT CTGCTTGCCG AACTTTCTCA	1320
40	ATAAACCTTA TTTCTTATTT ATAAAAAAA AAAAAAAA AAAAAA	1366

45 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

55	GCAGTAATTC CTGTTAGCCA CTGCATCCAC CAAACTAGT TTATTTTTC CCTCAAATTC	60
	ATGATTTTTA CGTCTGTTAC AAAGGGAATT TTGCTGATAG CTCTTTGGGT CCCACTGTTT	120
60	CATTTTATGC TAATAGATTC CATCTAGGG CCCAGCCGTC TCTTGACTGA TGGTGTTCCT	180

	TTTAACCCCTT GGCATGTATA ATAGAATTTT GGTGAATGAA AGAACCCAAA TAGGCCAGAT	240
	AGTCCCCCCA GGGCCTGATA TCCATAAAAG GCTTGGGAAT GCATTATGTA ATTGTCCTTA	300
5	GTCTTTTGT TGTTTTAGAA AAAAAACA AGATGGGCTC AGATGGATGC CTACGTAAAA	360
	ATGGTTCCTA GCTGTGTA CTAACTTTT CTTTGAATG AGTAGTGAAA GGAAGGAGGA	420
10	GGAAAGGAAA TTAAATGTCC TTCTAGTATT CTCTGGACTC AAGTCTGACA TATGAGATAA	480
	TAACCTATAT TGAAATGCCA AGAATTGTAT CTGAAACAAG AGAACAGTTT GACACATTTA	540
	TCATGCCTTC ATATTACATA TTAAGTAAA CCAATTAATA AACATATGAA ATATCCATG	600
15	CACAAGGCAA AGGCACCTAA ACCTTTTGT TCTTTTCTA CATAGCAGAA ATTGATTTTT	660
	TTTTTATTTT TTTAGGGGAA CCTATATAAT TATGACCCAG TGATGTCTTT TGGTGACTTA	720
20	AGCTTATGAA TTCAGGTTAC AATTGAGTTG ATTCTAGATG GTTACTACCT TGAAAAGGAT	780
	GTTGGTGCCT TATGTGACAC GAGCCAGAGC CTGCTGGGGA ATAAACAAAG CAGGTTTCAT	840
	GCCAACACCA ACTCGTAGCT TTAGTGGGCA GATGGGGAGT GGTTCACAGA CTTCCCAAAA	900
25	TGTGGGGGCT TTGGGATTTT CCACACCATC CCACGTGTGT TGTTCATTCT TCCTCTTTTC	960
	ACACTCTTGG ATGGATWATT TGRAAATGGT GRAAWYMMCY YYKRAATTTG CCCAATAGCC	1020
30	WTGRGCCACC ATTCTTWATG ACACCATAAC CAAATAGTTC CWTAAATGTTG AAATATTAGA	1080
	AACCTGTTAC CAGCCYKSMA KTWACCCWVA WTTTTCCTAT GTTTGTGGAA TTGATATTGA	1140
	AATAGCAGGG CTAAGGAATT ACTGGCAAGT TTAGCCTGT GGGTAATACC TTAGGGTTAT	1200
35	TTAAATATTT GTAATTTTAT TTAAATGTTT ATGAATGTTT GAAAGGAACA AAATTATCAG	1260
	GGATGGCTCT TGCCATGGG TCTTATTTTC ACCCTCTTTT CTGTAAGAAA AAAGAACAAT	1320
40	GTCTTAATGT ATTTTAAAG TTTTGGTAT AGTTTCTAAT TCCAATTTTA ATAAAAGTTT	1380
	TWRTAAAAA AAAAAAAAAA AAAAA	1405

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(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

55

CGGATTTTCT AGGACCCCAA AAAAAAAAAA AGGGNAAAAA AAACCCNCAA AACCANCCAA 60

AACCCCAAAA AAAAAAAAAA TCCACAAAAA CAAAAAACT ATAAAAAGA AAGAATTAAA 120

60

AACTTTCAGA GAATTACTAT TTACTTTATT AACTTACGGA TTTATTATAT AAATATATAT 180

TCACCTAGCA ACATATCTCT GCCGTCTCTC CTGCTCTCAT AATGAAGACA TAGCCGATTC 240
 TCTGCCCGGG CCCCTTGCTG ATGCTCCTCC GGGTCTGCGT CGGGCGTGGG TCTCTGGGA 300
 5 CCTCCAGAG GTGGAGGTGG GCTGATGCC TGGCTGCCTG GTGGTGTATG GTTTTGCTCC 360
 CCTACCTTT TTTTTTGAG TTTATCTGA TTGATTTTTT TTCTTGGTTT CTGGATAAAC 420
 10 CACCCTCTGG GGACAGGATA ATAAACATG TAATATTTTT AAGAAGGAAA AAAAAAAAAA 480
 AAAAACTNG GGGGGGCCCC CGAA 504

15

(2) INFORMATION FOR SEQ ID NO: 52:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

NAAGTATCTT GGCCAGTTTA TTACAGAGGA CGATAAATGA TTCCATGTGG ATAGGGCATA 60
 ACATACAGAG AATGAGACTA TGCCAGAAAT GGGAGGAGGC ATTTGAAACA ACATGAGTAT 120
 30 CTCAGGGACA GATGGATTGA TTCTGCTATT GGTAGGCCTG GAAGCAANGG TCAGAAGTAG 180
 CAAAAATGG ATACCAAAG CACTATTWGT CACCCAAGCT AAGTGAATA GCTGGCCCAG 240
 35 TAGGAGAAAT GCAGGTTTTG CTCTACACTA AGTCTCTCAA CTCTTGATAA GCCTCCAAAA 300
 ACAAATGTTA GGGGAAAAAA ACGCAGCTGG TTATGAAAAG ATATATCTCA TTTCATTAAA 360
 AAATCAATGT CAATGCTGTT AATAGAATCC TTTTATCTTC AGGACAGAGG CAATGCCCTA 420
 40 AACAAACACC AGCTCAAGAG CCTCTGATGC CAACCTAGAG GGTACCCAAA CACAACTTA 480
 GCATAGAGGT AAGAATCTCT ATGTCTTTTG GTGGAGGCAA AGCCATTTGG TTGGTACTTC 540
 45 ACAGGAACAT CTTTCTACCA AGTCTTCATC ATATGGTATG TGCCACGAGT CTCCAGTTGT 600
 TTGCACCACT GTGTCATAGC TGAGAATACG CTGAAAGGTT AGTTTTGATC CTGGAAACCT 660
 ATTTACAATT GCCAGCTGAT GTCCCTGCTG CCACTTAAAA AAGGCTTGGG TCTGGCATAG 720
 50 GCAGAMAGGC CTGTGGTCCC CTCGTGCCGA TTCTNGGCTC GAGGCCAATT NCCTTAT 777

55

(2) INFORMATION FOR SEQ ID NO: 53:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

5
ATGACTACAG TGTATACCC TCCAATCTTT GCAGGTGGG ATGGAACACT GCTTGATCA 60
CTCTGTGCAC GGTATAAATC CATATATCCA CAAAAACACA CATCCATCCA TCAACATATA 120
10 CATGGTTTGG GATGAGCAGG TCAATAGTTT TGAGAGGGAG TTTGTTCCCTT TTTTCTTCT 180
CATTATACTC TTAAATTGTT GTCAGTTATC AAACAAACAA ACAGAAAAAT TGTTTGGAAA 240
AACCTTGCAT ACGCCTTTTC TATCAAGTGC TTTAAATAT AGACTAAATA CACACATCCT 300
15 GCCAGTTTTT TCTTACAGT ACAGTATCCT TACCTGCCAT TTAATATTAG CCTCGTATTT 360
TTCTCACGTA TATTACCTG TGAATTGTAT TTGTTATTTA AACAGGAAAA AAAACATTCA 420
20 AAAAAAGAAA AATTAACTGT AGCGCTTCAT TATACTATTA TATTATTATT ATTATTGTGA 480
CATTTTGGAA TACTGTGGAA GTTTATCTC TTGCATATAC TTTATACGGA AGTATTACGC 540
CTTAAAAATA CGAAAATAAA TTTTACAAGG TTCCGGTTTT GGTGGTGGAA AGAGTAAATT 600
25 GA 602

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

40 ATGCACTGAC TTGGAGCCGC TCGGGGAAG TCCCGCCAG ACAGGCGTG GGTGGGAATG 60
CCTCACTTCA GTTTGAAGAG GGTCCGATC CAAAGGGTT AAAACGAGCG AACCCGATC 120
45 CCCGACCACA CTTCCCGCCT CCCTAAAACG CACACCCGC TAGCCATGGG CAGCCGCGAC 180
CACCTGTTCA AAGTGCTGGT GGTGGGGAC GCCGAGTGG GCAAGACGTC GCTGGTGCAG 240
GATTATTCCC AGGACAGCTT CAGCAAACAC TACAAGTCCA CGGTGGGAGT GGATTTTGCT 300
50 CTGAAGGTTT TCCAGTGGTC TGAATACGAG ATAGTGCGGC TTCAGCTGTG GGATATTGCA 360
GGGAGGAGC GCTTACCTC TATGACACGA TTGTATTATC GGGATGCCTC TGCTGTGTT 420
55 ATTATGTTTG ACGTTACCAA TGCCACTACC TTCAGCAACA GCCAGAGGTG GAAACAGGAC 480
CTAGACAGCA AGCTCACACT ACCCAATGGA GAGCCGGTGC CTGCCTGCT CTGGCCAAC 540
AAGTGTGATC TGTCCCTTG GGCAGTGAGC CGGGACCAGA TTGACCGTT CAGTAAAGAG 600
60

	AACGGTTTCA CAGGTTGGAC AGAAACATCA GTCAAGGAGA AAAAAAATAT TAATGAGGCT	660
	ATGAGAGTCC TCATTGAAAA GATGATGAGA AATTCCACAG AAGATATCAT GTCTTTGTCC	720
5	ACCCAAGGGG ACTACATCAA TCTACAAACC AAGTCCTCCA GCTGGTCCTG CTGCTAGTAG	780
	TGTTTGGCTT ATTTTCCATC CCAGTTCTGG GAGGTCTTTT AAGTCTCTTC CCTTTGGTTG	840
10	CCCACCTGAC CATTTTATTA AGTACATTG AATTGTCTCC TGACTIONGT CCAGTAAGGA	900
	GGGCCCCATG TCACCTAGAA AAGACACCTG GAACCCATGT GCATTTCTGC ATCTCCTGGA	960
	TTAGCCTTTC ACATGTTGCT GRCTCACATT AGTGCCAGTT AGTGCCCTCG GTGTAAGATC	1020
15	TTCTCATCAG CCTCAATTT GTGATCCGA ATTTTGTGAG AAGGATTAGA AATCAGCACC	1080
	TGCGTTT TAG AGATCATAAT TCTCACCTAC TTCTGAGCTT ATTTTCCAT TTGATATTCA	1140
20	TTGATATCAT GACTTCCAAT TGAGAGGAAA ATGAGATCAA ATGTCATTTT CCAAATTTCT	1200
	TGTAGCCGT TGTTCAGAT TCTTCTGTG TTGGAATGTA AACATCTGAT TCTGGAATGC	1260
	AGAAGGAGGG GTCTGGGCAT CTGTGGATTT TTGGCTACTA GAAGTGTCCC AGAAGTCACT	1320
25	GTATTTTGA AACTTCTAAC GTCATAATTA AGTTTCTCTT GTCTTGCCAT CAAGAATAGT	1380
	CAAGTTTTT GGCCGGGCAT GGTGGCTCAT GCCKGTAATC CCAGCACTG GGGAGGCCAA	1440
30	GGCAGGCGGA TCACATGAGG CCAGGAATTC GAGACCAACC TGGTCAGCAT GGCAAAACCC	1500
	CGTCTCTACT AAAAGTACAA AAATTAGCCA GCGTGATGG CAGTGTCTG TAATCCCAGC	1560
	TACTCTGGAG ACTGAGGTGG GAGAATCGCT TGAGACTGGG AGGCAGAGGT TGCAGTGAAC	1620
35	CGAGATCATG CCACCGCACT TCAGCCTGGG TGACAGAGAA GGACTCCGTC TCAAAAAAAA	1680
	AAAAAAAAA AAAACTCGAG GGGGGGCCCG GTACCCAAAT CGCCSTGATA GTGATCGTAW	1740
40	ACAATCNA	1749

45 (2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

55	AAAGAGATGG GCTCTTTATT TTCTCGAAAA ACCAATTTGG AGTTACTCAT TTTCCATAA	60
	CATTAAATTT CTTACAGTGA ACTACATATT GTCCATAAGT GCTTCATCAG GACTCATCGC	120
	CCTCCTGTCT ACTGGCTCCA AATAGACCAT GTCAGCTTCA CCCCCTGGCT TTGTGTCTAT	180
60	GGGTGGCCTG TGGTATATGG AAAAGTAGCA GGTGGTCAG GGTGGGAGAC ACAAGATGTT	240

	TTTATAGTCT AGAGCCTTTA AAAAACCAG CAGAATGTAA TTCAGTATTT GTTTATGGC	300
5	TGTTTTTTGA CAGATTGTG AATTAAATG AATTGAAAGG GAAACTCAGA GTAGTAGGAC	360
	GTTTATTAAA AGGAAAAAAA TGTCTTGCAA TGTGCTGTAA TCACAAGAGG AGAAAAAAC	420
	TTGTTTCCTT GATCTGTCAG AGGTCACAGT AACCTGGGCC GAGCTGTTAT TATTTATTAT	480
10	ATAATAGTAG TAGGAAGTTA ATAACCTGGT CTCTGTGTTT CAAGCACAAT ATTACAACCT	540
	CTTTTGAACC GTAAATATCA GAATGAATCC TCTTCCCAGG GGATTGAACA GAAGCTTAAT	600
15	GTTTACAAGT GTTTGAATTT GTGATCTGAA ATAACACAAA ATTAAAAACA TGATTTCTCT	660
	AATTTTCCAA CTAGAGGAAG AGAACTTGT GGAAAAGTTC TTTTITTTTC TTTTITTTT	720
	CTTAAAGAAG GGCAGCCAAG GTAGTAACCT AAAAATAGTG CCCAGGCATA TGAGAGTTGT	780
20	CCTACGAGGT TAAAGAACAC ACTGTTCCAC TGTATGGCTT TGGCCCTGAG TGGCCAGGGA	840
	GGTCAACTTG ACCCTGCCAT GTTGGTTTGA CTTACTAAGA CACAGGAATC ATTGTTTTC	900
25	TTGACCAGGG TCTCACACCC TGGAGGAATG TTAAGTAAGA GAAAGAACCT CTTTCTGAA	960
	TATTGACATG TAAAAGACCA AAGTAATTTT TCTGAACTTC TGCAATTCTG AGAACTCTCC	1020
	AAGGAATTTA CAGTGATTTT AGTGCTTGTC AGCATTTTTC CATGAGGACT TTCATACATT	1080
30	TGACTCTTTA GTTCACAGGT TCCCATTGAT TGTGAGCAAG ATATTTATCT CTTTAGCCCT	1140
	TGGGATCCA GCTGAGAGCA ATCTCTTGCA TTTTTTTACC CGTGATGTA CAGATATCAT	1200
35	TTCTGTGTA TGCCATGACT TGAAAAAGTT TGGGAAGCTC TTTAGCAATA TCAGCTAAAA	1260
	GGATATGAAA TCACAGGTGA TAGCAGTTGT CATTCACTAA TTTCTTACAA GCAGCACCCC	1320
	AAAGGAAATA TAGTCCTAAT CTTTACTATC CACTTCTAAA TTTAATGTGA ATTTCATACA	1380
40	TGTTATTAGT TGTTTCTTTT ATAATTTTAT AAAAATTATT CATCGGGAGT TTAACCTCCA	1440
	CTTCCATGCT ATCGGATGTG TTGGGCTCCA TGCAAGAACT TGAAGAAAA ACAGGCAGGA	1500
45	ATGCATTTGC ATAATGACCC AGATCATCAT TTTCTGCAAC TGAGAATTAT ATTTTCATCAT	1560
	TGCTTCTAGA AGTCTGCAAT TCTTTACTTT TCTTTGGTGC ATTATTATCT AGGTGCCATC	1620
	ACTGGATAAT GTGGAGTGAC TAGAGAAGTC AYATATCACT GTAAGGTACA GTTAGGGGTA	1680
50	ACACTTTAGA GGTTTATTAT TTTTAAAAA CTTTCTTGA ACTCCTGGGC CAACATGGGT	1740
	GAAACCCCGT CTTCTTACTT AAAAATACCC AAAATTAGGC CAGGGGCGTG GATGGGTGGG	1800
55	GTGCCTGTTA ATCTTCAGCT ACTTNGGGGA GGGCTTGAAG CCAGGGAGGA ACTGCCCTGG	1860
	ANCCCCGGGG NGGGCCAGNA GGTTCGCCAG TTGAGT	1896

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

10 TCTTTTAAAT ATAGACATTT GTGGGGCTCA CACAATATAT GAAATAGTAC CCTCTAAAAA 60
 AGAGAAAAAA AAAATCAGGC GGTCAAACCT AGAGCAACAT TGTCTTATTA AAGCATAGTT 120
 15 TATTTCACTA GAAAAAATTT AATATCAAGG ACTATTACAT ACTTCATTAC TAGGAAGTTC 180
 TTTTAAAT GACACTTAA ACAATCACTG AAACTTGAT CCACATCACA CCCTGTTTAT 240
 20 TTTCCCTTAA CATCTTGGA GCCTAAGCTT CTGAGAATCA TGTGGCAAGT GTGATGGGCA 300
 GTAAAAATACC AGAGAAGATG TTTAGTAGCA ATTAAAGGCT GTTTCACCT TTAAGGACCA 360
 GCTGGGCTGT AGTGATTCCT GGGGCCAGAG TGGCATTATG TTTTACAAA ATAATGACAT 420
 25 ATGTCACATG TTTGCATGTT TGTTCCTTG TTGAATTTTT GAACAGCCAG TTGACCAATC 480
 ATAGAAAGTA TTACTTTCTT TCATATGGTT TTTGGTTCAC TGGCTTAAGA GGTTCCTCAG 540
 AATATCTATG GCCACAGCAG CATACCAGTT TCCATCCTAA TAGGAATGAA ATTAATTTTG 600
 30 TATCTACTGA TAACAGAATC TGGGTCACAT GAAAAAAAT CATTTTATCC GTCTTTTAAG 660
 TATATGTTTA AAATAATAAT TTATGTGTCT GCATATTGCA GAACAGCTCT GAGAGCAACA 720
 35 GTTTCCTATT AACTCTTCT GACCAATAGT GCTGGCACC GTCCTCCTC TTTGGGAAGA 780
 GGAAAGGGTG TGTGAACATG GCTAACAATC TTCAAATACC CAAATGTGA TAGCATAAAT 840
 AAAGTATTTA TTTTATGCCT CAGTATATTA TTATTTAATT TTTTAGGTAA TGCCTATCTC 900
 40 TTGGTCTATT AAGGAAAGAA GCAATCAGTA GAGAATTCAG GATAGTTTIG TTTAAATTCT 960
 TGCAGATTAC ATGTTTTTAC AGTGGCCTGC TATTGAGGAA AGGTATTCTT CYATACAACT 1020
 45 TGTMTTAAAC TTTGAGAACA TTGACAGAAA TTATGCAATG GTTTGTTGAG ATACGGACTT 1080
 GATGGTGCTG TTTAATCAGT TTGCTTCCAA AGTGGCTAC TCAAGAGGCC CTAAGACTGG 1140
 TAGAAATTAA AAGGATTTCA AAAACTTTCT ATTCCTTTCT TAAACCTACC AGCAAACCTAG 1200
 50 GATTGTGATA GCAATGAATG GTATGATGAA GAAAGTTTGA CCAAATTTGT TTTTGTGTG 1260
 TTGTGTGTGT TTGAATTTG AAATCAITCT TATTCCTTTT AAGATGTTT ATGTATGAGT 1320
 55 GTGAAGATGC TAGCGAACCT ATGCTCAGAT ATTCATCGTA AGTCTCCCTT CACCTGTTAC 1380
 AGAGTTTCAG ATCGGTCCT GATAGTATGT ATTTCTTTAG TAAGAATGTG TTAATAATTAC 1440
 AATGATCTTT TAAAAAGATG ATGCAGTTCT GTATTATTG TGCTGTGTCT GGTCTAAGT 1500
 60

GGAGCCAATT AAACAAGTTT CATATGTATT TTTCCAGTGT TGAATCTCAC ACACTGTACT 1560
 TTGAAAAATT CCTTCCATCC TGAATAACGA ATAGAAGAGG CCATATATAT TGCCTCCTTA 1620
 5 TCCTTGAGAT TTCACTACCT TTATGTTAAA AGTTGTGTAT AATTGTTAAA ATCTGTGAAA 1680
 GAATAAAAAG TGGATTTAAA TTAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1740
 10 AAAAAAAGG GGG 1753

15 (2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

25 GCGGAAGTTA CTGCAGCCGC GGTGTTGTGC TGTGGGAAG GGAGAAGGAT TTGTAAACCC 60
 CGGAGCGAGG TTCTGCTTAC CCGAGGCCGC TGCTGTGCGG AGACCCCGG GTGAAGCCAC 120
 CGTCATCATG TCTGACCAGG AGGCAAAACC TTCAACTGAG GACTTGGGGG ATAAGAAGGA 180
 30 AGGTGAATAT ATTAACTCA AAGTCATTGG ACAGGATAGC AGTGAGATTC ACTTCAAAGT 240
 GAAAATGACA ACACATCTCA AGAACTCAA AGAATCATAC TGTCAAAGAC AGGGTGTTC 300
 35 AATGAATTCA CTCAGGTTTC TCTTGAGGG TCAGAGAATT GCTGATAATC ATACTCCAAA 360
 AGAACTGGGA ATGGAGGAAG AAGATGTGAT TGAAGTTTAT CAGGAACAAA CGGGGGGTCA 420
 TTCAACAGTT TAGATATTCT TTTATTMTT TTTCTTTCC CTCAATCCTT TTTTATTMTT 480
 40 AAAAAAGTT CTTTGTAAAT GTGGTGTICA AAACGGAATT GAAACTGGC ACCCATCTC 540
 TTTGAAACAT CTGGTAATTT GAATCTAGT GCTCATTTAT CATTATTGTT TGTMTTCATT 600
 GTGCTGATTT TTGGTGATCA AGCCTCAGTC CCTTCATAT TACCTCTCC TTTTAAAAA 660
 45 TTACGTGTGC ACAGAGAGGT CACCTTTTTC AGGACATTGC ATTTTCAGGC TTGTGGTGAT 720
 AAATAAGATC GACCAATGCA AGTGTTCATA ATGACTTTCC AATGGCCCT GATGTTCTAG 780
 50 CATGTGATTA CTTCACTCCT GCACTGTGAC TTTCACTGGG AGATGGAAGT TTTTCAGAGA 840
 ACTGAACTGT GGAAAAATGA CCTTTCCTTA ACTTGAAGCT ACTTTTAAAA TTTGAGGGTC 900
 TGGACCAAAA GAAGAGGAAT ATCAGGTTGA AGTCAAGATG ACAGATAAGG TGAGAGTAAT 960
 55 GACTAACTCC AAAGATGGCT TCACTGAAGA AAAGGCATTT TAAGATTTTT TAAAAATCTT 1020
 GTCAGAAGAT CCCAGAAAAG TTCTAATTTT CATTAGCAAT TAATAAGCT ATACATGCAG 1080
 60 AAATGAATAC AACAGAACAC TGCTCTTTTT GATTTTATTT GTACTTTTTG GCCTGGGATA 1140

TCGGTTTAA ATGGACATTG TCTGTACCAG CTTTATTAAA ATAAACAATA TTTGTAAAAA 1200
TCAWAAAAAA AAAAAAAAAA 1220

5

(2) INFORMATION FOR SEQ ID NO: 58:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1049 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

TCGCGCCTGC AGACACAGCA TCTACTCAGC GTGGGTCACC TCTGTGAACA TCACTGACTG 60
CAAGCCTCCC TCAATTTCTG GTGCAGCCCA TCAGGGACCC ACAGCGCCTG GGAGGATGGT 120
GCGGATCTTG GCCAATGGGG AAATCGTGCA GGACGACGAC CCCCAGTGA GGACCACTAC 180
25 CCAGCCACCA AGAGGTAGCA TTCTCGACA GAGCTTCTTC AATAGGGGCC ATGGTGCTCC 240
CCCAGGGGGT CCTGGCCCCC GCCAGCAGCA GGCAGGTGCC AGGCTGGGTG CTGCTCAGTC 300
CCCCTTCAAT GACCTCAACC GGCAGCTGGT GAACATGGGC TTTCCGAGT GGCATCTCGG 360
30 CAACCATGCT GTGGAGCCGG TGACCTCCAT CCTGCTCCTC TTCTGCTCA TGATGCTTGG 420
TGTTCTGGC CTCTCCTGG TTGGCCTTGT CTACCTGGTG TCCCACCTGA GTCAGCGGTG 480
35 ACCTCTGAGG GCTGATAGGG GTGGGTTTGT TGAGAGGGAC TTGCTGGGCC TTGGTGTGAG 540
AGCAGGCATA TTTGGAGGGG ATCTGGTGGT GCCTTGAAGG TATGATCAGA GAGGGGACCA 600
CAGGTGTGTG TTTCCCTTTT GTGTTAAGCG TGAGGCAGAG GGAGACGTTA GTCCAGCAT 660
40 TTCCCAAAGT GTGGGTGGT CCGTTGGTTC CCGAGATACT TTTAGGTGGT ATGGGGCCTG 720
CATTAAAGTG CACAAAATCA GAGCAAGAAA GCGATGCCCT TCCCAATTCT CTCAATCCTT 780
45 TTATGCCGAG AAGATCTCAG CTGGATGCCA ACATGTTCCG ATGCCTGTGG AAGACATGCC 840
GACGTCTCCT CTGCCTAGGG AGCAGGACTT GGGCTTAGGG CAGGTGGAAG AAATTCAGA 900
CTTTTITAGC ACTGTTTTTG TTITAATGGT ATATTTTAT TGGCTACTTT ATTGTTTAGG 960
50 ACAAGTGGTA GTGGCATTCT ATTTATGTG ACCTTTTCAA TAAATAGATT TAAGTAAAAA 1020
AAAAAAAAA AAAACTCGAG GGGGGGCC 1049

55

(2) INFORMATION FOR SEQ ID NO: 59:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

	AAAGAGGATG TGMAGCTAGA GGTCCCCGAT GGCTGGTCGG ATGGGAAGCA CAAGGCTGAG	60
10	GGACTGGATT GTAAAGGCAC TAAGTCGTTT TCGGTGAGA ATCAGACATG GGGGACCTCT	120
	AGCTTCACAT CCTCTTTCTT TGCAGSTCTG GACATCCTGA GCCCAAGTCC CCCACACTCA	180
15	GTGCAGTGAT GAGTGCAGAA GTGAAGGTGA CAGGGCAGAA CCAGGAGCAA TTTCTGCTCC	240
	TAGCCAAGTC GGCCAAGGGG GCAGCGCTGG CCACACTCAT CCATCAGGTG CTGGAGGCCC	300
	CTGGTGCTTA CGTGTTTGA GAACTGCTGG ACATGCCCAA TGTTAGAGAG CTGGCTGAGA	360
20	GTGACTTTGC CTCTACCTTC CGGCTGCTCA CAGTGTTCG TTATGGGACA TACGCTGACT	420
	ACTTAGCTGA AGCCCGGAAT CTTCTCCAC TAACAGAGGC TCAGAAGAAT AAGCTTCGAC	480
25	ACCTCTCAGT TGTCAACCTG GCTGCTAAAG TAAAGTGTAT CCCATATGCA GTGTTGCTGG	540
	AGGCTCTTGC CCTGCGTAAT GTGCGGCAGC TGGAAGACCT TGTGATTGAG GCTGTGTATG	600
	CTGACGTGCT TCGTGGCTCC CTGGACCAGC GCAACCAGCG GCTCGAGGTT GACTACAGCA	660
30	TCGGGCGGGA CATCCAGCGC CAGGACCTCA GTGCCATTGC CGAACCCTK AANAAAAACC	720
	ATTAAAGTTA CGACGGCAGC AGCAGCCGCA GCCACATCTC AGGACCCTGA GCAACACCTG	780
35	ACTGAGCTGA GGAACCAGC TCCTGGCACC AACCAGCGCC ASCCAGCAAG AAAGCCTCAA	840
	AGGGCAAGGG GCTCCGAGGG ANCGCCAAGA TTTGGTCCAA GTCGAATTGA AAGRACTGTC	900
	GTTCCTCCC TGGGGATGTG GGGTCCCAGC TGCCTGCCTG CCTCTTAGGA GTCCTCAGAG	960
40	AGCCTTCTGT GCCCCTGGCC AGCTGATAAT CCTAGGTTCA TGACCCCTCA CCTCCCCTAA	1020
	CCCCAAACAT AGATCACACC TTCTCTAGGG AGGAGKCAA TGTAGGTCAT GTTTTGTGTTG	1080
45	GTACTTTCTG TTTTGTGTA CTTCATGTGT TCCATTGCTC CCCGCTGCCA TGCTCTCTCC	1140
	CTGTCTTCCT TAAGAGCTCA GCATCTGTCC CTGTTCATTA CATGTCATTG AGTAGGTGGG	1200
	TAGCCCTGAT GGGGTCGCT CTGTCTGGAG CATAACCCAC AGGCGTTTTT TCTGCCACCC	1260
50	CATCCCTGCA TGCCTGATCC CCAGTTCCTA TACCCTACCC CTGACCTATT GAGCAGCCTC	1320
	TGAAGAGCCA TAGGGCCCCC ACCTTTACTC ACACCCTGAG AATTCTGGGA GCCAGTCTGC	1380
55	CATGCCAGGA GTCAGTGAC ATGTTTCATC TAGAATCCTG TCACACTACA GTCATTTCTT	1440
	TTCTCTCTC TGGCCCTTGG GTCCTGGGAA TGCTGCTGCT TCAACCCAG AGCCTAAGAA	1500
	TGGCAGCCGT TTCTTAACAT GTTGAGAGAT GATTCCTTCT TGGCCCTGGC CATCTCGGGA	1560
60	AGCTTGATGG CAATCCTGGA AGGGTTAAT CTCCTTTTGT GAGTTTGGTG GGAAGGGAA	1620

GGGTATATAG ATTGTATPAA AAAAAAAAAAG GTATATATGC ATATATCTAT ATATAATATG 1680
 ACGCAGAAAT AAATCTATGA GAAATCTATC TACAAAMWAA AAAAAAAAAA AAAAAAAAAA 1740
 5 AGGAATTCGA TNTCAAGCTT ATCGATACCG TCNACC 1776

10

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACAGATAAAT AAATAAATAA TAAATTAAAT TAAATAAAAA ATCTGAGCTA ATCTGAATAA 60
 ATTGAGAGAT TTCACATGAA AGCCAGGATT TCTGGCTTCC CAGGAACAGT CAGAAGAGCT 120
 25 AGCTAGCAAC ACTGGTCTGC TTGGCTACCT TCTTTGGAAC AACATGAAAT CTAGCTCCCT 180
 TTTTTTTTTT TTTTGGCCC ACTTCATCCA TTCACATGAC CTGCTGGCC TCTGCAGGTA 240
 AGTGAGTATG CAACAAAAAT GTAGCACAGG TTTTGTGCT GAACTACGTG GTTTCAGGTC 300
 30 CAGCTCTGCC ACTTGCTAGC ATGACCTCGT GCCGAATTCC NGCACGAAGT TTTTTTTTTT 360
 TTTTTCAGTG CTCCAGTCCC CCTATTGGAG AATCCTGCCC CCCCCTGGGA CAGAATGTTC 420
 35 ACCCTGGCCC CGCGANTCCC TGA 443

40

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 2888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

50 TTAATGTTGT CAATAACCAC CAGGCCAAAC AGAATTTATA TGACCTGGAT GAAGATGATG 60
 ATGGTATAGC TTCCGTTCCCT ACTAAACAGA TGAAGTTTGC AGCCTCAGGC GNCTTTCTCC 120
 ACCACATGGC TGGGCTAAGC AGTTCCAAGC TTTCATGTC CAAGGCCCTC CCTCTCACCA 180
 55 AAGTGTTTCA GAATGATGCA TACACAGCTC CTGCTCTCCC TTCTCTATT CGAACAAAAG 240
 CCTTGACCAA CATGTCCCGG AACTGGTGA ACAAGGAAGA ACCCCCCAAA GAGCTGCCAG 300
 60 CTGCTGAGCC TGTCTCAGC CCATTGGAAG GCACCAAGAT GACTGTGAAT AATCTGCACC 360

	CTCGAGTCAC TGAGGAGGAC ATTGTTGAGC TTTTCTGTGT GTGTGGGGCC CTCAAGCGAG	420
5	CTCGACTGGT CCATCCTGGG GTAGCGGAGG TGGTGTTTGT GAAAAAGGAC GATGCCATCA	480
	CCGCATATAA GAAGTACAAC AACCGGTGTC TGGACGGGCA GCCGATGAAG TGCAACCTTC	540
	ACATGAATGG GAATGTTATC ACCTCAGACC AGCCCATCCT GCTGCGGCTG AGTGACAGCC	600
10	CATCAATGAA AAAGGAGAGC GAGCTGCCTC GCAGGGTGAA CTCTGCCTCC TCCTCCAACC	660
	CCCCTGCGA AGTGGACCCT GACACCATCC TGAAGGCACT CTTCAAGTCC TCAGGGGCCT	720
15	CTKTGACCAC GCAGCCACCA GAATTCAAAA TCAAGCTTTG AGCAGGGGAG TGAGGCAGCC	780
	AGAAGTGGG GCAGAGGAGG GTGGCTCTGT TTCCCAAGG CAAAGCTTAT GACCAATGGG	840
	CCATCGGACT GGAGACCCCT GATTGTGGGA AGGGTTGCCA GGGATAAAGA GCTTCCTCAC	900
20	TGGATGGGAC CCGCCTTTCT GTGTGTGTT CTGCCCTGTG CTCTTCTCTC TACGTTAAGC	960
	TTTCTGTAG TATGTTTCTT CATCTCATCG CCAAGGTAGG CTTGTGTTTT TCAGTGTGTG	1020
25	CCTCCCCGAG CCTCAGCCCC AAGCTGATTT CTTATCTGGA AATGGTACAC TGAATCTCT	1080
	GGGTGGCTTT CTTGTGGCCC CATGGGATGC AGCGTGGGG CTGTCTGAAG GACCCTGCTT	1140
	TTTCCAGGG CCGAGGGGCT GCCTTTCCTT TGTGTGTATT AAGCTTTTCA AACAAATGGAG	1200
30	GGGATGGAGA GCCCTGGTGT CCTGACGGGA GCCAGGTGG CCTGAGAGCT GTGCCGCTCC	1260
	TCTGTCTGT CAGTGGAGGT GCCTGGGTGG GGAGCAGGTC TCAGGCCTCT TGTCTCTCC	1320
35	CCAGTGGCTC CAGGCCTCAC TAGTGGCAAG GGCAGGATGA GGCTGCACCG CTGGGAAGAG	1380
	TCTATCTAAG YTCTTGGCTT GGAGTCCCGT GTCGTCTCCR CCCAGAGGAA GTTCTCCAGA	1440
	GTTACCTTT CCCTTTTCCT TGAGTTGTGC TGAATGCCCC ACCCCAGCTC TCTTTCCCTT	1500
40	CTGGGTGTCT TTGCTGGGAG GGGGCTGTGT TGTGAGCCCT CCCGGTTCTC ACCTCGCCTG	1560
	GCACTTAACC ACACCCTGGT TTTGTGTAGC CGCCAGCTCT CTTCTGGTTG GGCCTTTGAA	1620
45	AGGCTCAGCC TCCCATGTG CAGTGCTTGG GTTTGGAGCT TATTTGAATG GAAGAGGTCA	1680
	GTTTGTTCCT GGCTCTCCAT TTCTGGCCTC AGTTGTCTAC AGGACAGTGG TCAGGGATGC	1740
	CTGGAGGCAT ATATCCAGCT GCCACCAAGG GGCAGTGTG GTTCCACTT ATGTGAGTGA	1800
50	CCCCATCCAT CCATGACCAG AGGATTATTT TCCTGCCTTG GCAGAGGAGG AGGAGTCAAG	1860
	GGAGCAGGGC AGCTCTACCA GGCAAGGTGT TTCCCCAGCA TAGGCGCAGA CAGTTGGGAC	1920
55	GAAACTTCAG AGCCCAGGCA GTCCCTGAAT GACCAGGCCA GTGTTGTCAC TGAGTGGTCC	1980
	CCTGCTGTTT GGGAGTGAAG AGAATCCAG CTGGCAGAGC TGGAGCCAGT TGGGGAGCAC	2040
	GGTTCTGGGA GCTCTGCAAA ATCAGTAGCA AGTGCTGGAA AAGGCACATG CCGAAGATAC	2100
60	TCAAGAGCTC CCAAGATTTG CTTGAGGCTA GCCCAGTGAA RAAAACCAGA GACTCATGTT	2160

	TCCAGGGGTC AGTCTGTCAG GCAGGAAGGA CCCAGGATTT GAACCCAGCT TCAGTGTGCA	2220
5	GGCTCTGAGG CTGCCCAGGA CGGGAAAGTC CAAGGAAGGG GCCTGGTGGT GCTCCACTTG	2280
	CAGTTCTTTA AAGAATGCTG CTTTTTATTC TCCTAACCCCT TTCAAGTGGG TGCAGACTTC	2340
	TCGTTAGCAG CTGGAAGACA TTCCTCCAC ACTTTTCCCT TCCTGGCCCA AGAGAGCATC	2400
10	CAGAAGGCAG TAGGACCTGG TTTTTCAGGT ACTGGGAGCC GGGGGCTCAC TGCTTGCACT	2460
	GTGCTTAGGG TAGGGATGGT AAATATCCTC CCTGCATGGC TTTATCCTCC CTCTCATCCC	2520
15	AAAGCAGGTA TCTTCTGGTT GTCACAGAGT TTCATTGAGT CCAGCTGCAG CCACGTGGCC	2580
	ATCTGGAGCT GGTGCTATAG GTGACCATCT GGTACATTGA GGGGACCTGT TTGCCTCCTC	2640
	CACTCTATAA GCAGTCATCT TGGGAGACCG GGAGGAGAAG GTGGTGGGCT AGTCCTGTGT	2700
20	CCTCCTCCAC TTCCCATGCC TCTATGTTAC CCATCTGTGT CTCCTGTGCA GAAGGAGAGG	2760
	AAGGGGCATT AAGAGATGAA GGGTGATTAT GTATTACTTA TCCATTTCTG AATAAACATT	2820
25	TGTTATTCCT AAAAAAAAAA AAAAAAACT CGAGGGGGGG CCCGGWACCC AWATCGCCSK	2880
	AAAGTGAG	2888

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(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

	CACTAGTATA ATTTATAATT ATAACCTATT CTGATTTCTT TTCAAATATT AGGTGTCCTA	60
	GTTGCCTATG AAGGTTTGCC ACTTCATCTT GCACTGTTCC CCAAACCTTG GACTGAGCTA	120
45	TGCCAGACTC AGTCTGCTAT GTCAAAAAAC TGCATCAAGC TTTTGTGTGA AGATCCTGTT	180
	TTGCGAGAAT ATATTAAATG TATCCTAATG GATGAAAGAA CTTTTTTTAA CAACAACATT	240
50	GTCTACACGT TCATGACACA TTTCCTTCTA AAGGTTCAAA GTCAAGTGTT TTCTGAAGCA	300
	AACGTGCCA ATTTGATCAG CACTCTTATT ACAAACCTGA TAAGCCAGTA TCAGAACCTA	360
	CAGTCTGATT TCTCCAACCG AGTTGAAATT TCCAAAGCAA GTGCTTCTTT AAATGGGGAC	420
55	CTGAGGGCAC TCGCTTTGCT CCTGTCAGTA CACTCTCCA AACAGTTAAA CCCAGCTCTA	480
	ATTCCAACCTC TGCAAGAGCT TTTAAGCAAA TGCAGGACTT GTCTGCAACA GAGAACTCA	540
60	CTCCAAGAGC AAGAAGCCAA AGAAAGAAAA ACTAAAGATG ATGAAGGAGC AACTCCCAT	600

AAAAGGCGGC GTGTTAGCAG TGATGAGGAG CACACTGTAG ACAGCTGCAT CAGTGACATG 660
 AAAACAGAAA CCAGGGAGGT CCTGACCCCA ACGAGCACTT CTGACAATGA GACCAGAGAC 720
 5 TCCTCAATTA TTGATCCAGG AACTGAGCAA GATCTTCCTT CCCCTGAAAA TAGTTCTGTT 780
 AAAGAATACC GAATGGAAGT TCCATCTTCG TTTTCAGAAG ACATGTCAAA TATCAGGTCA 840
 10 CAGCATGCAG AAGAACAGTC CAACAATGGT AGATATGACG ATTGTAAAGA ATTTAAAGAC 900
 CTCCACTGTT CCAAGGATTC TACCCTAGCC GAGGAAGAAT CTGAGTTCCC TTCTACTTCT 960
 ATCTCTGCAG TTCTGTCTGA CTTAGCTGAC TTGAGAAGCT GTGATGGCCA AGCTTTGCCC 1020
 15 TCCCAGGACC CTGAGGTTGC TTTATCTCTC AGTTGTGGCC ATTCCAGAGG ACTCTTTAGT 1080
 CATATGCAGC AACATGACAT TTTAGATACC CTGTGTAGGA CCATTGAATC TACAATCCAT 1140
 20 GTCGTACAAA GGATATCTGG CAAAGGAAAC CAAGCTGCTT CTGACATTA GGTGTAGCAT 1200
 GTCTACTTTT AAGTCCCTCA CCCCCAACC CCATGCTGTT TGTATAAGTT TTGCTTATTT 1260
 GTTTTGTGC TTCAGTTTGT CCAGTGCTCT CTGCTTGAAT GGCAAGATAG ATTTATAGGC 1320
 25 TTAATTCTTG GTCAGGCAGA ACTCCAGATG AAAAAAAGT GCATCTTCAG TATACTTCCT 1380
 AAAGGCAAT CAGATAATGG ATATGTTTTA TGTAAATTAAG AGTTCACCTT AGTGGCTTTC 1440
 30 ATTTAATATG GCTGTCTGGG AAGAACAGG TTGCCTAGCC CTGTACAATG TAATTAAAC 1500
 TTACAGCATT TTTACTGTGT ATGATATGGT GTCTCTGTG CCAGTTTGT ACCTTATAGA 1560
 GGCAGATTGC CTCGATCCC TGTGTTCTT ATTATCAAAA TTAAGTTTAC TTGTATACGG 1620
 35 AACAACCACA AGAAATTTGA TTCTGTAAAG AATCCTCTTT AGCTGTGGCC TGGCAGTATA 1680
 TAAATGGTGC TTTATTTAAC AGAATACCTG TGGAGGAAAT AAAGCACACT TGATGTAAAA 1740
 40 ATAATTGTTT TATTTTATT GACATGACTG ATTGATTGCT ATTCTGTGCA CTTAATTAAA 1800
 CTGATTGTGA TGACTTWWAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A 1851

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(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 3542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

60 TCCAATGCTG ATGAGCGTCT TCGCTGGCAG GCCAGCTCCT TGCCTGCTGA TGACCTTTGC 60
 ACAGAAAATG CCATCATGCT GAAACGATTC AATAGGTATC CGCTGATCAT TGACCCCTCT 120
 60 GGACAGGCCA CAGAATTCAT TATGAATGAA TATAAGGWTG GTAAGATCAC ACGGACCAGC 180

	TTCTGGATG ACGCCTTCAG AAAGAACTTA GAGAGTGCAC TGAGATTTCG TAACCCCTT	240
5	CTGGTCCAGG ATGTGGAAAG CTACGATCCA GTTTTGAACC CGGTGCTGAA CCGTGAAGTG	300
	CGGCGAACAG GGGGGAGAGT GCTGATCACT CTCGGGGACC AGGACATAGA CCTGTGCCA	360
	TCGTTTGTC TCTTCTGTC CACCCGGGAT CCAACTGTG AGTTCACC AGATCTCTGT	420
10	TCCCGGGTTA CTTTTGTAAC CTTCACAGTT ACCCGTAGCA GTTTACAAAG CCAGTGTCTA	480
	AATGAAGTAC TTAAGCAGA AAGACCTGAT GTGGACGAGA AACGATCTGA TCTTCTTAAA	540
15	CTTCAAGGGG AATTTTCACT CCGTTTGGCT CAGCTGGAAA AATCTCTACT ACAAGCTCTG	600
	AACGAGGTGA AAGGGCGCAT TTTGGATGAC GACACGATCA TAACCACTCT GGAGAACCTG	660
	AAGAGAGAGG CTGCAGAGG CACCAGGAAA GTTGAGGAGA CGGACATTGT CATGCAGGAG	720
20	GTGGAGACCG TGTCCAGCA GTACCTCCCG CTCTCCACCG CCTGCAGCAG CATCTACTTC	780
	ACCATGGAGT CCCTCAAGCA GATACACTTC TTGTACCACT ACTCCCTCCA GTTTTTCCTG	840
25	GACATTTATC ACAACGTCT ATACGAGAAC CCGAACCTGA AGGGTGTAC CGACCACACA	900
	CAGCGCTGT CCATTATAAC AAAGGACCTC TTCCAGGTGG CGTTTAACCG AGTGGCTCGA	960
	GGCATGCTGC ATCAGGACCA CATTACCTTT GCCATGCTGC TGGCAAGAAT CAACTGAAG	1020
30	GGCACCGTG GGGAGCCAC CTACGATGCA GAATTCAGC ACTTCTTGAG AGGAAATGAG	1080
	ATTGTCTGA GTGCTGGCTC CACCCCAGG ATCCAGGGCC TGACTGTGA GCAGGCGGAG	1140
35	GCGGTGGTGA GGCTGAGCTG CCTTCCCGG TTTAAGGACT TGATTGCAA GGTTCAGGCA	1200
	GACGAGCAAT TTGGCATCTG GCTGGACAGC AGCTCCCGG AGCAGACTGT GCCCTACCTC	1260
	TGGAGTGAAG AAACACCTGC AACACCCATT GGCCAGGCCA TCCACCGCT GCTCCTGATC	1320
40	CAGGCTTTCC GGCCGATCG CCTGTTGGCC ATGGCCACA TGTTTGTTTC AACAAACCTT	1380
	GGGAGTCTT TCATGTCCAT CATGGAGCAG CCGCTCGACC TGACCCACAT TGTGGSCACA	1440
45	GAGGTGAAGC CCAACACTCC TGTCTTAATG TGCTCTGTGC CTGGTTATGA TGCCAGTGGA	1500
	CATGTCGAGG ACCTTGACG CGAGCAGAAC ACGCAGATCA CTTCAATTGC AATCGGCTCT	1560
	GCAGAAGGCT TTAACCAAGC AGATAAGCA ATAAACACCG CTGTAAAGTC GGCAGGTGG	1620
50	GTGATGCTGA AGAATGTGCA TCTGGCCCCA GGGTGGCTGA TGCAGCTGGA GAAGAAGTTG	1680
	CATTCCTGC AGCGCATGC CTGCTTCCGA CTCTTCTCA CCATGGAGAT CAACCCAAG	1740
55	GTGCCTGTA ATCTGCTCCG TCGGGCCGC ATCTTTGTGT TCGAGCCACC GCCAGGKTG	1800
	AAGGCCAACA TGCTGAGGAC GTTCAGCAGC ATTCCGCTCT CACGGATATG CAAGTCTCCC	1860
	AACGAGCGTG CCCGCTGTA CTTCTGCTG GCCTGGTTTC ATGCGATCAT CCAAGAACGC	1920
60	TTACGATACG CACCACTGGG GTGGTCAAAG AAGTATGAAT TTGGAGAGTC TGACCTGCGG	1980

	TCANYTTGCG ATACGGTGGA CACGTGGCTG GATGACACGG CCAAGGGCAG GCAGAACATC	2040
5	TCACCGGATA AGATCCCGTG GTCTGCACTA AAGACCTTAA TGGCCAGTC CATTTATGGC	2100
	GGGCGCGTGG ACAACGAGTT TGACCAGCGT CTGCTCAACA CCTTCCTGGA GCGCCTGTTT	2160
	ACAACCAGGA GTTTCGACAG TGAGTTTAAG CTGGCATGCA AGGTCGACGG ACATAAAGAC	2220
10	ATTCAAATGC CAGATGGCAT GCAGGCGAGA GGAGTTTGTG CAGTGGGTGG AGTTGCTCCC	2280
	CGACACCCAG ACGCCCTCCT GGCTGGGCCT GCCCAACAAC GCCGAGAGAG TCCTCCTTAC	2340
15	CACACAGGGT GTGGACATGA TCAGTAAAAT GCTGAAGATG CAGATGTTGG AGGATGAGGA	2400
	CGACCTGGCC TACGCAGAGA CTGAGAAGAA GACGAGGACA GACTCCACGT CCGACGGGCG	2460
	CCCTGCCTGG ATGCGGACAC TGACACCAC CGCGTCCAAC TGGCTGCACC TCATCCCCCA	2520
20	GACGCTGAGC CACCTCAAGC GCACCGTGA GAATATCAAG GATCCTTTGT TCAGGTTCTT	2580
	TGAGAGAGAA GTGAAGATGG GCGCAAAGCT GCTTCAGGAC GTTCGCCAGG ACCTTGAGA	2640
25	TGTCGTCCAG GTGTGCGAAG GAAAGAAGAA GCAGACCAAC TACTTGCGCA CGCTGATCAA	2700
	CGAGCTAGTG AAAGGGATCT TGCCTCGGAG CTGGTCCCAC TACACGGTGC CTGCCGGCAT	2760
	GACCGTCATC CAGTGGGTGT CCGACTTCAG CGAGAGGATC AAACAGCTGC AGAACATCTC	2820
30	ACTGGCAGCT GCATCTGGTG GCGCCAAGGA GCTAAAGAAC ATCCACGTGT GCCTGGGTGG	2880
	CCTGTTCTGT CCTGAGGCGT ACATCACTGC CACCAGGCAG TATGTGGCCC AGGCCAACAG	2940
35	CTGGTCCCTG GAGGAGCTCT GCCTGGAAGT CAACGTCACC ACCTCACAGG GCGCCACCCT	3000
	TGACGCTTGC AGCTTCGGAG TCACGGGTTT GAAACTTCAA GGGGCCACGT GCAACAACAA	3060
	CAAGCTGTCA CTGTCCAATG CCATCTCAAC CGCCCTTCCC CTGACGCAGC TCGCTGGGT	3120
40	CAAGCAGACA AACACCGAGA AGAAGGCCAG TGTGGTAACC TTACCTGTCT ACCTGAACCT	3180
	CACCCGTGCA GACCTCATCT TCACCGTGA CTTCGAAATT GCTACAAAGG AGGATCCTCG	3240
45	CAGCTTCTAC GAGCGGGGTG TCGCAGTCTT GTGCACAGAG TAAACTTTTC TAGCTGCCCC	3300
	TTTCTGTAAT AGTGAAAGTT GGTATTTAAC ATTTATTCAT TTTTAAAATA TTTGGAAGGT	3360
	CTGAGCTTGT GAAAAGAAAAG TGGTTGGTCT GAGGTTGGAG GAAGCTGAAT GGAATCTGAC	3420
50	GGTTGGGAGT GGTGGAAATT GGAAGGATAC CAGGAGGTAT TTGGGAAGGC CAATGGCGTG	3480
	GCTCCTTTGA GGAAATAAAA CACTAAGCAT GAAAAAATAA AAAAACTTA CAANCCNCAA	3540
55	GG	3542

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

5 AGGTGATTTT AATGATAGGT GTCATATATA GGACGGATAA TCTGTTTACA TTCTGTTCTT 60
 10 CTCGATGCAC TCACAAGCGG GTAAGTAGGT GACAAGAAAA CAAAGATCTT ATTCAAAAGA 120
 GGTCTTACAG CAACCCAACG TCTCATCTTC CCATAGTAAA GATGACGGCG CCTTGAGGTA 180
 15 AGCTACAGGC AACACCACTT CCGCGTTTCT CTGCGCCCT GGTCCAAGAT GGCGGATGAA 240
 GCCACGCGAC GTGTTGTGTC TGAGATCCCG GTGCTGAAGA CTAACGCCGG ACCCCGAGAT 300
 20 CGTGAGTTGT GGGTGCACCG ACTGAAGGAG GAATATCAGT CCCTTATCCG GTATGTGGAG 360
 AACACAAGA ATGCTGACAA CGATTGGTTC CGACTGGAGT CCAACAAGGA AGGAACTCGG 420
 TGGTTTGAA AATGCTGGTA TATCCATGAC CTCCTGAAAT ATGAGTTTGA CATCGAGTTT 480
 25 GACATTCCTA TCACATATCC TACTACTGCC CCAGAAATTG CAGTTCCTGA GCTGGATGGA 540
 AAGACAGCAA AGATGTACAG GGGTGGCAAA ATATGCCTGA CGGATCATTT CAAACCTTTG 600
 30 TGGGGCCAGG AATGTGCCCA AATTGGACT AGCTCATCTC ATGGCTCTGG GGCTGGGTCC 660
 ATGGSTGGCA GTGGAAATCC CTGATCTGAT TCAGAAGGGC GTCATCCAAC ACAAAGAGAA 720
 ATGCAACCAA TGAAGAATCA AGCCACTGAG GCAGGGCAGA GGGACCTTTG ATAGGCTACG 780
 35 ATACTAWTTT CCTGTGCATC AACTTAACT CATCTAACTG TTCCCCGGAC ANCCTCCACT 840
 CTAGTTGTTA CTAAGTANTG CAGTAGCATT NTGGGAAGA ACA 883

40

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1541 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

45 GGCACGAGGT GGCCTCTACC CTGGGCTCAT CTGGCTACAC AGGGACTCTA AACGCTTCCA 60
 55 GATTCCCTGG AAACATGCCA CCCGGCATAG CCCTCAACAA GAAGAGGAAA ATACCATTTT 120
 TAAGGCCTGG GCTGTAGAGA CAGGAAGTA CCAGGAAGGG GTGGATGACC CTGACCCAGC 180
 TAAATGGAAG GCCCAGCTGC GCTGTGCTCT CAATAAGAGC AGAGAATTCA ACCTGATGTA 240
 60 TGATGGCACC AAGGAGGTGC CCATGAACCC AGTGAAGATA TATCAAGTGT GTGACATCCC 300

TCAGCCCCAG GGCTCGATCA TTAACCCAGG ATCCACAGGG TCTGCTCCCT GGGATGAGAA 360
 5 GGATAATGAT GTGGATGAAG AAGATGAGGA AGATGAGCTG GATCAGTCGC AGCACCATGT 420
 TCCCATCCAG GACACCTTCC CCTTCTGAA CATCAATGGT TCTCCCATGG CGCCAGCCAG 480
 TGTGGGCAAT TGCAGTGTGG GCAACTGCAG CCCGGAGGCA GTGTGGCCCA AAAGTGAACC 540
 10 CCTGGAGATG GAAGTACCCC AGGCACCTAT ACAGCCCTTC TATAGCTCTC CAGAACTGTG 600
 GATCAGCTCT CTCCCAATGA CTGACCTGGA CATCAAGTTT CAGTACCGTG GGAAGGAGTA 660
 15 CGGGCAGACC ATGACCGTGA GCAACCCTCA GGGCTGCCGA CTCTTCTATG GGGACCTGGG 720
 TCCCATGCCT GACCAGGAGG AGCTCTTTGG TCCCGTCAGN CTGGAGCAGG TCAAATTCCC 780
 AGGTCTGTAG CATATTACCA ATGAGAAGCA GAAGCTGTTC ACTAGCAAGC TGCTGGACGT 840
 20 CATGGACAGA GGAAGTATCC TGGAGGTCAG CGGTATGCC ATTTATGCCA TCAGGCTGTG 900
 CCAGTGCAAG GTGTACTGGT CTGGGCCATG TGCCCCATCA CTTGTTGCTC CCAACCTGAT 960
 TGAGAGACAA AAGAAGGTCA AGCTATTTTG TCTGGAAACA TTCCTTAGCG ATCTCAATTGC 1020
 25 CCACCAGAAA GGACAGATAG AGAAGCAGCC ACCGTTTGAG ATCTACTTAT GCTTTGGGGA 1080
 AGAATGGCCA GATGGGAAAC CATTGGAAG GAAACTCATC TTGGTTCAGG TCATTCCAGT 1140
 30 AGTGGCTCGG ATGATCTACG AGATGTTTTC TGGTGATTTC ACACGATCCT TTGATAGTGG 1200
 CAGTGTCCGC CTGCAGATCT CAACCCAGGA CATCAAGGAT AACATCGTTG CTCAGCTGAA 1260
 GCAGCTGTAC CGCATCCTTC AAACCCAGGA GAGCTGGCAG CCCATGCAGC CCACCCCCAG 1320
 35 CATGCAACTG CCCCCTGCCC TGCCTCCCCA GTAATTGTGA ATGCCATCTT CTTCCTTCTC 1380
 TTTTITATAA TATGTACAT ATGGATTTT TTATTGTTA GATTTAACCA GCTTTTAAAT 1440
 40 CTCTGTTTTT TGTGACAGTG TTAGAAGTTT GTGATTCTCC AAATATGCCT AGATTTAAAG 1500
 CTGATTTAAT TTATGAAAAA AAAAAAAAAA AAAAAAAAAA A 1541

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(2) INFORMATION FOR SEQ ID NO: 66:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 732 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAAAAATGAA TGTTAGAAGG TGCTGCCGA GCGGGACAG AGTGTGCT CGCGCTGGAG 60
 AAGGCTCTGC TCAGCCCTGA GAGTCCCTTC CTGCCCCACC GATACTGGCA CTTTAAAAAG 120
 60

GAAGCTGACC GCACAGTGTC CAGACGAATT GGCCCCCAGA AGATGGGGAG TTCTGTCTCTG 180
CCCTTCTGTG TCTGCGTGAC CTCACCCAGC CTAGGAGGGA GGTGCATTCA GGGTAGATTT 240
5 GCCTCTCATT CAAAGTTCTG GGGCTTTGGG CGGAAAACAG CCAGCTTTGG CGCTGTTGGG 300
GAGACTCCTC CAGACCAGGA ACCCCAGAAG GAGACAGAGC CTGCCACATC CTCCCACGCC 360
10 AGGCCCTGGG CCAGGGTGAT TGGACTGAGA ATTTGGCCAC AACCAAATTG ATGCTGGCTG 420
GAACCAGAGG CCAGAAAGCC TGGCCTTGTC CCCATGTGGG AGCCCTGTCC TCAGCCCTCT 480
TGTCCCTTG AGCTCAGTGA ATTCCCACCA GGTGCCACA GCTCCTGGAC TTCAAATTCT 540
15 ATATATTGAG AGAGTTGGAG AGTATATCAG AGATATTTT GGAAAGGAGT TGGTCTATGC 600
AATGTCAGTT TGAATCTTC TTGAAAGTTT AATGTTTTTA TTAGGAGATT TAAAGAAAAT 660
AAAGTCTAC AATATCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720
20 AAAAAAAAAA AA 732

25

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

35

TTAAGGAATT CGGCMCGATC CCGCAAGTA ACATGACTAA AAAGAAGCGG GAGAATCTGG 60
GCGTCGCTCT AGAGATCGAT GGGCTAGAGG AGAAGCTGTC CCAAGTGTGG AGAGACCTGG 120
40 AGGCCGTGAA CTCCAGACTC CACAGCCGGG AGCTGAGCCC AGAGGCCAGG AGGTCCCTGG 180
AGAAGGAGAA AAACAGCCTA ATGAACAAAG CCTCCAATA CGAGAAGGAA CTGAAGTTTC 240
45 TTCCGCAAGA GAACCGGAAG AACATGCTGC TCTCTGTGGC CATCTTTATC CTCCTGACGC 300
TCGTCTATGC CTAAGTGACC ATGTGAGCCT GGCATTCCC CACAACCAGC ACAGGCTTCC 360
ACTTGGCCCC TTGGTCAGGA TCAAGCAGGC ACTTCAAGCC TCAATAGGAC CAAGGTGCTG 420
50 GGTGTTCCTC CTCCCAACCT AGTGTTCAGG CATGGCTTCC TGGCGGCCCA GGCCTGCTCT 480
CCTGGCCTG CTGGGGGTT CCGGCTCTCC AGAAGGACAT GGTGCTGGTC CCTCCCTTAG 540
CCCAAGGGAG AGGCAATAAA GAACACAAAG CTGAAAAAA AAAAAAAAAA AACTCGTAGG 600
55 GGGGGCCCGT ACCCAATCGC CCTNTCTGTG 629

60

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

10 CTGCTAGCCG GCCGGCGCAG GCTGCCGAGC GGGTGAGCGC GCAGGCCAGG CCAAAGCCCT 60
GGTACCCGCG CGGTGCGGGC CTCAGTCTGC GGCCATGGGG GCGTCCGCGC GGCTGCTCGG 120
15 AGCGGTGATC ATGGGGGCCC CGGGCTCGGG CAAGGGCACC GTGTCGTGCG GCATCACTAC 180
ACACTTCGAG CTGAAGCACC TCTCCAGCGG GGACCTGCTC CGGGACAACA TGCTGCGGGG 240
CACAGAAATT GGCGTGTAG CCAAGGCTTT CATTGACCAA GGGAACTCA TCCCAGATGA 300
20 TGTCACTACT CGCTGGCCC TTCATGAGCT GAAAAATCTC ACCCAGTATA GCTGGCTGTT 360
GGATGGTTTT CCAAGGACAC TTCCACAGGC AGAAGCCCTA GATAGAGCTT ATCAGATCGA 420
25 CACAGTGATT AACCTGAATG TGCCCTTTGA GGTCAATAA CAACGCCTTA CTGCTCGCTG 480
GATTCATCCC GCCAGTGGCC GAGTCTATAA CATTGAATTC AACCTCCCA AACTGTGGG 540
CATTGATGAC CTGACTGGGG AGCCTCTCAT TCAGCGTGAG GATGATAAAC CAGAGACGGT 600
30 TATCAAGAGA CTAAAGGCTT ATGAAGACCA AACAAAGCCA GTCCTGGAAT ATTACCAGAA 660
AAAAGGGGTG CTGGAACAT TCTCCGAAC AGAAACCAAC AAGATTTGGC CCTATGTATA 720
35 TGCTTTCCTA CAACTAAAG TTCCACAAAG AAGCCAGAAA GCTTCAGTTA CTCCATGAGG 780
AGAAATGTGT GTAACATTA ATAGTAAGAT GGGCAAACCT CCTAGTCCTT GCATTTAGAA 840
GCTGCTTTTC CTAAGACTTC TAGTATGTAT GAATTCCTTG AAAATTATAT TACTTTTATT 900
40 TCTACTGATT TTATTTTGA TACTAAGGAT GTGCCAAATG ATTCGGATAC TAAGATGCAT 960
CGTTTGAAAT CATCTAGTGT GTTGATGCA GTTATCCTCA AAAACATCAG CGATGTCTGA 1020
45 ACCTTTAAAA CATCTGTTAG AGCAAAATTA AAAGAGCATT TGGTAGTAAT CTAACTTTTT 1080
GTTCAATTAA TAAGTGGTTG ATAAAGTTTC CATATTTTTTC TGGAAAAGTT AAAAAAGTT 1140
ACATGTCATT TGGAGAAAAT ACCTAATCAG AAATTTGTGC ATAGATTGAT GCCAAAAAG 1200
50 ACATTTCCAG CATTTGTGAA CATGGTGAGA CACTATATAA AATTCCAGAA AGAAAGCAAC 1260
TGGATTTACA GATTTATTGT GAGACACAAA TTCACTGCTG CCTTTACACT AAGAAATGTA 1320
55 TATGTTAACC ATATATGCTG TATTTATTTT GTCGTTAAGC ATACTTTCAG TTTACTCAGA 1380
ATTTTCAATT TGCTATAAAG ATGTATCAAT TAGCATATAG AAAAATATTA CTTTAAGATG 1440
ACTTGTTCCT TTTGAAAATA CCTGTGTAAT GAGGGTTATG ATTTGTGTCA AAAATTGACA 1500
60

TAAGTGCTTT TACAAGCACC AAAGTTGAAT GAATTTTCAA CAAAATGTAA TTAAAGTCTA 1560
 TGTTTTCAGT TATGACTCAG GTTAAGAAAT GTGTTTtagg ATCTACTTGC TGGTTTttct 1620
 5 TTTTGATCCA AATGTGTGAT CTGCCCTGAT AAATAACAAG TTATNGTACC ATCTCCCCCG 1680
 CCAATAAAAA AAAAAAAAAA AAAAAAAAAAC TCGAGGGGGG GCCCGGTACC CAATTCTCCG 1740
 10 NAATAGGNAG T 1751

15 (2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 508 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

25 GGCACGAGAT TATGTATTAA AATGTTTTTG AATGTGAAA TATTAGAATA TTGTTACTAT 60
 TTGACCCAAC TCAAAATCTC CATGGGAAAA TACCTGTCGA TACCCACAGT ATTGTTGAAA 120
 ATAATCAGAT GCAGTATCAC AGCTGTGTCA GACTCTAGTA CCAGTTGGGC AATCAAGGCA 180
 30 CAGCTAAAAA TTGAAAACAA AGATCTGGAC AACAAAACAG CCAAAGGTGG GGTCAAGAA 240
 GCTCTGACGT GTACCTAGCT GTAGAATGCT ATGCACACGT GCCAGGTGTA GTGTGCATAT 300
 35 CCAGGAAAAA CTGCAGAGAG CCCAGTCTT CACCTCTGGT TGACCATGAG CTCTGTGTAA 360
 GCAGGAAGTG AAGGCTAAGG CAGATTTAAG CTCTGAAAGC ATTCCACAAC ATACACACAA 420
 ATCGTGCAAA GCATTAAGGA AATCTTGTTA CTGCTAAGTG TTGCTGACCC AGGAACAAC 480
 40 CCTACTCAGC TGGACTTAAA AATAAAAA 508

45 (2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 245 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

55 TACATAGAGC AAAGAGAAAT TTCCAGAATT TCTARAATTC TGGAAAGAGA ATTTTCCTGA 60
 GATTGCAGAT TTGCTTGTGT CCTCAGGTGA TGATAGGGC TGTMTTCCCC TGTGTCCCTT 120
 60 TCCTCACACT CATGCTTCCT CTCCTAGAGT GTCTGGTTGG CATGATCATG TGCTACCTAG 180

GCATTTCTTT CACTGATACA AGGAAACTG CAGGGTTAAA AAAAAAAAAA AAAAAAAAAA 240
NCNCG 245

5

(2) INFORMATION FOR SEQ ID NO: 71:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATGTTCTCTCA TGAGGATGCA CTGTGCTTC TGCAAGTATT GCTGCAGCTT CATAGTGACT 60
20 CCCACCAGCA CCAGCAATAC AGCTAGCTAC CTGTGGCCTT GGATCTCAGC CAGCATGGCT 120
GGGAGAGGGA GCAGCTGGGC ATGTACCCTA AATGCTGTTA CCAGGGAAGG ACTCCCAGAG 180
TGAAGACAAG TAGGGACTTC CTGCAGAGGT GGTACATGTG CTCTCTGTAT CCATACTTTT 240
25 TTTTTTTTTT TTTTGAGATA GAGTTTCACC CTTGTTGCCC TGGCTGGAGT GCAATGGTGC 300
GATCTCAGCT CACTGCAACC TCTCTGCCTC CCGGGTTCAA GTGATTCTCC TGCCTCAGCC 360
30 T 361

35

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

45 AGGATCACAC AATAGAGAAC ACTGTAGTAA CATTTCCGTC TGCTCACAAG ACCCAGAACA 60
TTGATCAGTT TTTGTTGTTG GTTTATTATT TTCTGTAA AAAATTGTGA AAAGTTTGT 120
TTAGCTAGAT GATATTTTAA TAGCTGCGAG TGCTTTGGAA CTATAAAGAT GTCACTACTT 180
50 AACACACATA CCTTATGTTT TGTGTTGTTT TGTGTTTACAC TCAGTATAAA TCAGGAGAAG 240
TTAGCCAACC ATCTAGCATT TAGAATCCTC TTTTATTATG TCTTCTAAGG ATATGGATGT 300
55 TCCCATAACA GCAACAAAAC AGCAACAAA ACATTTTCATA AATATCACTT GATAGACTGT 360
AAGCACCTGC TTAACCTTGT GTCCCAAATA TTTAGTGTGT ATATATATAT ATATATATAC 420
ACACACACAC ACATATATAT TCAACAAAATA AAGCAAAATA TAACATGCAT TTCACATTTT 480
60

GTCTTTCCCT GTTACGATTT TAATAGCAGA ACTGTATGAC AAGTTTAGGT GATCCTAGCA 540
TATGTTAAAT TCAAAATTAAT GTAAAACAGA TTAACAACAA CAAAGAAACT GTCTATTTGA 600
5 GTGAAGTCAT GCTTTCTATT ATAATAACTT GGCTTCGGTT ATCCATCAAA TGCACACTTA 660
TACTGTTATC TGATTGTTTA TAATAAGAA TACTGTACTT ATAAAAAAAA AAA 713

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(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GAAAGTCAGA GCTGTCCAAT CCCTCAGCAC CTTTGTAGATT TGCTCCAAAT TAGAAACGTG 60
GGGACTATGT GTTCTGGGCA ATCAGAGGTC TGGAAAATGG CTCTGCAGGC TCTTGATAGT 120
25 GAGACAGTGG TCATCTTACC AGACATGCAT CTGATTTTAA GCCTCAGGCT AATCCACAAT 180
GCTCGGCCAT GCCTATGATT AACAAACAAA AGCAAAATCT GCTTTTATAG TTTAGGAAAC 240
30 CTGGATAGAA CAGTATTTTT CAGCATTTCTT GGATAAAGCA GTTCTGCATT TTTAAATTGG 300
GACTGCAGAA GTGACTGTCT ATAGTTGTGA AATACAAAAA ATGGTATGTT TGATCAGAAA 360
AGGAAGCCCG TGCCTGGCAC TTGGAAAGAT ACTGAGCATC ATAACCCTAA TGAGAAAATG 420
35 TAGGCTCTGT GAATGTTAAC TACAAATCAG GTTAGGAAAG CATATGACAC CCTTTGTCAA 480
ACTAAGCTTC ACTAGGAGGA CCTGTGCTCA TAGAAGAATA TGCTTTAAAA GTATCAATTT 540
40 TCCACAGTCG ATGATGGAGA AAAGTTCATT TGCACCAGAA TGCTGATAGT CACAATACAC 600
AGCCTGACAT ATATACAAT ACAGTTTTCT GTAAACAGAA GTTCTTCCTC TTCCAATTCA 660
GGAGTCAGTC AGAGCATAAA TATGTCATGT TTCCTTTAG AAACGATTC ATTTTAGAAA 720
45 GCAGATCTGG ATTATTTTGC AGGGTAGAAA TGAAGGCTAT TTCTGGCATT CTTGCTCAA 780
AAGTCAATAT ATGTACATTA AGTATAAAAA AGGGTCTCTT TCACCTCTTT TGTTCGTAG 840
50 CATTCGCTAC ATAACTCGTG CC 862

55 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 4602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

5	GCGAGGGGGC GKGGGGAGCA GCGCCGARGC CGCCGCCTCC GCCTCCGCCG CCTAGGACTA	60
	GGGGGTGGGG GACGGACAAG CCCCAGTGCC GGGGGAKACG GAAGAGCCGA GACCCCGGA	120
10	GCAGCAGGAC CAGGAAGGGG GAGAGGCGGC CAAGCGGCT CCGGAGGACC CGCAACAACG	180
	CCCCCTGAG GCGGTGCGG CGGCGCCTGC AGGGACCACT AGCAGCCGCG TGCTGAGGGG	240
	AGGTCCGGAC CGAGGCCGG CCGCTGCGRC CGCCGCGCMG CAGCTGTGTC CCGCCGAGA	300
15	AGGCCGAGTA TCCCCGCCG CGAGGAGCAG CCCAGCGCC AGGCCTCCCG ACGTCCCCGG	360
	GCAGCAGCCC AGGCCGCGAA GTCCCCGTCT CCAGTTCAGG GCAAGAAGAG TCCGCGACTC	420
20	CTATGCATAG AAAAAGTAAC AACTGATAAA GATCCCAAGG AAGAAAAAGA GGAAGAAGAC	480
	GATTCTGCCC TCCCTCAGGA AGTTTCCATT GCTGCATCTA GACCTAGCCG GGGCTGGCGT	540
	AGTAGTAGGA CATCTGTTC TCGCATCGT GATACAGAGA ACACCCGAAG CTCTCGGTCC	600
25	AAGACCGGTT CATTCAGCT CATMTGCAAG TCAGAACCAA ATACAGACCA ACTTGATTAT	660
	GATGTTGGAG AAGAGCATCA GTCTCCAGGT GGCATTAGTA GTGAAGAGGA AGAGGAGGAG	720
30	GAAGAAGAGA TGTTAATCAG TGAAGAGGAG ATACCATICA AAGATGATCC AAGAGATGAG	780
	ACCTACAAAC CCCACTTAGA AAGGGAAACC CCAAGCCAC GGAGAAAATC AGGGAAGGTA	840
	AAAGAAGAGA AGGAGAAGAA GGAAATTAAA GTGGAAGTAG AGGTGGAGGT GAAAGAAGAG	900
35	GAGAATGAAA TTAGAGAGGA TGAGGAACCT CCAAGGAAGA GAGGAAGAAG ACGAAAAGAT	960
	GACAAAAGTC CACGTTTACC CAAAAGGAGA AAAAGCCTC CAATCCAGTA TGTCCGTTGT	1020
40	GAGATGGAAG GATGTGGAAC TGTCCTTGCC CATCCTCGCT ATTTGCAGCA CCACATTAAG	1080
	TACCAGCATT TGCTGAAGAA GAAATATGTA TGTCCCATC CCTCTGTGG ACGACTCTTC	1140
	AGGCTTCAGA AGCAACTTCT GCGACATGCC AAACATCATA CAGATCAAAG GGATTATATC	1200
45	TGTGAATATT GTGCTCGGC CITCAAGAGT TCCACAATC TGGCAGTGCA CCGGATGATT	1260
	CACACTGGCG AGAAGCATTA CAATGTGAGA TCTGTGGATT TACTGTGCGA CAAAAGGCAT	1320
50	CTCTTAATTG GCACATGAAG AAACATGATG CAGACTCCTT CTACCACTTT TCTTGCAATA	1380
	TCTGTGGCAA AAAATTGAG AAGAAGGACA GCGTAGTGGC ACACAAGGCA AAAAGCCACC	1440
	CTGAGGTGCT GATTGCAGAA GCTCTGGCTG CCAATGCAGG CGCCCTCATC ACCAGCACAG	1500
55	ATATCTTGGG CACTAACCCA GAGTCCCTGA CGCAGCCTTC AGATGGTCAG GGTCTTCCTC	1560
	TTCTTCCTGA GCCCTTGGGA AACTCAACCT CTGGAGAGTG CCTACTGTGA GAAGCTGAAG	1620
60	GGATGTCAAA GTCATACTGC AGTGGGACGG AACGGGTGAG CCTGATGGCT GATGGGAAGA	1680

	TCTTTGTGGG AAGCGGCAGC AGTGGAGGCA CTGAAGGGCT GGTATGAAC TCAGATATAC	1740
	TCGGTGCTAC CACAGAGGTT CTGATTGAAG ATTCAGACTC TGCCGGACCT TAGTGGACAG	1800
5	GAAGACTTGG GGCATGGGAC AGCTCAGACT TTGTATTIAA AAGTTAAAAA GGACAAAAA	1860
	AAAATCTAAA GCATTTAAAA TCTAGTGAAA TAACTGAAGG GCCTGCTCTT TCCATTGTGG	1920
10	ATCACAGCAC ACACATACAT ACACCTCCA CCTCCCCATC CCCTGTTCTC CCTCTGTTGC	1980
	TCCCCTTATA AAATTGATGT TGTCTTTACC AGAAAGGTAG ACAAAAAAGA AGCAGCAGCA	2040
	GCTCTTAAAG TGAGGGTTAT TCTCATACTC GGTTCAGCC ATCAGCAGAC TTCCTGCTCA	2100
15	TCGGCAGATC CCCCTTTCCA ACCTGTAACCT CTGATGTGCT CTGGATCAGC TTTTAACTTT	2160
	TAATCATATA TTACTGTCTT CTAAATCCCT TCTCCTCTC TACTGCTGCC CTATGGTTCT	2220
20	GGCTCCTACC CCTGCGGCA CACTTATCTT CAAATACCAT AGAATTCTAA TCTCTGAAAT	2280
	CATAGCTCTC CAGTGGCTTT TAAAGAAAGC TGGTCCTCAG CACTAACAAA ATCACTACAA	2340
	TAGCCTAGTG CTMTTTTGA AGCCTTTTGA GGAAGAATG TTAGGTTTAT GGTAAGTAGT	2400
25	ATGCTCTTTG AGATTTTAC AGTGTGAAA CTAAAGAATT TTGAGAGGGT GAGGAGGGTT	2460
	GTTCAGAATC TAAATTACAG ATAGATGATT GTTCTTGTG AATTGTGTTT TTTTCCTTTT	2520
30	TTTTGTCCC TACCATTTC TTACATTTC CTMTGGGCC ATCTCTGGCT CCTTGCTTTT	2580
	TGTTCTTGC TTTGCTTTAT CAGTTCATTC CAGCTCCCTG TTAGTGAAGG AACTGCTGT	2640
	TAGTGAAGGA ACAAAGTCTA TGAGTCCTAA AATTTTAAGT CAAAGAAAAC TGCTCTGTTT	2700
35	CCCCTTTAGT AACACTTCTG AAGAGGAAAA ACTTCAATAG CCAAAGTTAA TAATCTATA	2760
	TAATAATTGC TTTGGCTTTC ACCTAAAATT CTGGGCATCA CAATTTCCCT GGGATAGAGG	2820
40	TTGTGTGGG GAATAGATTG CTTATTGCTG TTCACTGGAG AGAAAAGGTA GTGTTTTTGT	2880
	ACAAGGTCAT ACCGCCAGAA GCCCCAAATC CTATTTTGGC TCATCTTCAG GTAAAGAGTA	2940
	ATTCCTATCC TGTGTGCCCTC AGAAGCTAGA ATCGAAGGCT TACCCTATTC ATTGTTTATT	3000
45	GTCAGAAATG CATGATGGCT CTTGGAAAGA ATGACGTTTT GCTGGAAAAA AAAAAAARA	3060
	CMGTTGTGT TTCACAAACA TGGCTTATCA ATTTTTTCAA AGAATTCTTT TTTCCCAAAA	3120
50	AGAGGAGTAA CAAAATGTCA TTTCTGAAAG AGGCTTACTT TATACCACT AGTGTACGCA	3180
	TTTGGGATGC CAGGGAACAG AGAGTGAGAC ACCTACAATC ACCAGTCTCA AATGCGCTAT	3240
	TGTTCTTTTT CAGAGTGTG CAGATTTGCC ATTTCTCCAT AATATGGGA TAGAAAATGG	3300
55	AATAAGATA GAAGGATGT AGAATATGCT TTCCTGCCAA CATGGTTTGG AGTCGACTTT	3360
	GGTATATTGA CTAGATTTGA AAATACAAGA TTGATTAGAT GAATCTACAA AAAAGTTGTC	3420
60	CTCCTCTCAG GTCCCTTTTA CACTTTTGA CTAAC TAGCA TCTATATTC ACACCTAGCT	3480

TTTTGTGCAC ACTTATCCTT TGTCTCCGTA AATTTTCATTT GCAGTGGTTA GTCATCAGAT 3540
 ATTTTAGCCA CCTACACAAA AGCAAACTGC ATTTTAAAA ATCTTTCTGA GATGGGAGAA 3600
 5 AATGTATTCT CTTTTCCTAT ACCGCTCTCC CAACAAAAAA ACAACTAGTT AGTTCTACTA 3660
 ATTAGAACT TGCTGTACTT TTTCTTTTCT TTTAGGGTC AAGGACCCTC TTTATAGCTA 3720
 10 CCATTGCGCT ACAATAAATT ATTGCAGCAG TTTGCAATAC TAAAATATTT TTTATAGACT 3780
 TTATATTTTT CTTTGTGATA AAGGGATGCT GCATAGTAGA GTTGGTGTA TAAACTATC 3840
 TCAGCCGTTT CCCTGCTTTC CTTCTGCTC CATATGCCCTC ATTGTCTTC CAGGGAGCTC 3900
 15 TTTTAATCTT AAAGTTCTAC ATTTTCATGCT CTTAGTCAA TTCTGTTACC TTTTAAATA 3960
 CTCTTCCAC TGCATATTTT CATCTGAAT TGGTGGTTCT AAATCTGAA ACTGTAGTTG 4020
 AGATACAGCT ATTTAATATT TCTGGGAGAT GTGCATCCCT CTTCTTTGTG GTTGCCCAAG 4080
 20 GTTGTTTTGC GTAACGTAGA CTCCTTGATA TGCTTCAGAG AATTTAGGCA AACACTGGCC 4140
 ATGGCCGTGG GAGTACTGGG AGTAAAATAA AAATATCGAG GTATAGACTA GCATCCACAT 4200
 25 AGAGCACTTG AACCTCCTTT GTACCTGTTT GGGGAAAAAG TATAATGAGT GTACTACCAA 4260
 TCTAACTAAG ATTATTATAG TCTGGTTGTT TGAATAACCA TTTTTTCTC CTTTGTGTT 4320
 TTTCCCACTT TCCAATGTAC TCAAGAAAAT TGAACAAATG TAATGGATCA ATTTAAAATA 4380
 30 TTTTATTTCT TAAAAGCCTT TTTTGCCTGT TGTAATGTGC AGGACCCTTC TCCTTTCATG 4440
 GGAGAGACAG GTAGTTACCT GAATATAGGT TGAAGAGTT ATGTAAAAAG AAATTATAAT 4500
 35 AAAAGGATA CTTTGCTTTT CAAATCTTTG TTTTCTCTTA TTCTAGGTAA GGCATATTAA 4560
 AAATAAATAT GTAAAGAAGA AAAATAAAG TTGTCTTCAT GG 4602

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(2) INFORMATION FOR SEQ ID NO: 75:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGCGCCCCGG GCCGGCGGGT TTCTTAACA AATAACAGA ACCCGCACTG CCCAGGCGAG 60
 CGTTGCCACT TTCAAAGTGG TCCCTGGGG GAGCTCAGCC TCATCCTGAT GATGCTGCCA 120
 55 AGGCGCACTT TTTATTTTTA TTTATTTTTT ATTTTTTTTT TAGCATCCTT TTGGGGCTTC 180
 ACTCTCAGAG CCAGTTTTTA AGGGACACCA GAGCCGAGC CTGCTCTGAT TCTATGGCTT 240
 60 GGTGTGTTACT ATAAGAGTAA TTGCCTAACT TGATTTTTCA TCTCTTTAAC CAAACTTGTG 300

5 GCCAAAAGAT ATTTGACCGT TTCCAAAATT CAGATTCTGC CTCTGCGGAT AAATATTTGC 360
 CACGAATGAG TAACTCCTGT CACCACTCTG AAGGTCCAGA CAGAAGGTTT TGACACATTC 420
 TTAGCACTGA ACTCCTCTGT GATCTAGGAT GATCTGTTCC CCTCTGGAT GAACATCCTC 480
 TGATGATCAA GGCTCCCAGC AGGCTACTTT GAAGGGAACA ATCAGATGCA AAAGCTCTTG 540
 10 GGTGTTTATT TAAAATACTA GTGTCACTTT CTGAGTACCC GCCGCTTCAC AGGCTGAGTC 600
 CAGGCCTGTG TGCTTTGTAG AGCCAGCTGC TTGCTCACAG CCACATTTCC ATTTGCATCA 660
 TTACTGCCTT CACCTGCATA GTCACCTTTT TGATGCTGGG GAACCAAAAT GGTGATGATA 720
 15 TATAGACTTT ATGTATAGCC ACAGTTCATC CCCAACCCCTA GTCTTCGAAA TGTTAATATT 780
 TGATAAATCT AGAAAATGCA TTCATACAAT TACAGAATTC AAATATTGCA AAAGGATGTG 840
 20 TGTCTTTCTC CCCGAGCTCC CCTGTTCCCC TTCATTGAAA ACCACCACGG TGCCATCTCT 900
 TGTGTATGCA GGGCTATGCA CCTGCAGGCA CGTGTGTATG CACTCCCCGC TTGTGTTTAC 960
 ACAAGCTGTG GGGTGTACG CATGCCTGCT TTTTTCACCT AATAATACAG CTTGGAGAGA 1020
 25 TTTTGTATC ACATTATAAA TCCCACTCGC TCTTTTGTAT GGCCACATAA TAACTACTGC 1080
 ATAATATGGA TACGCCTTAT TTGATTTAAC TAGTTCCTA ATGATGGACT TTTAAGTTGT 1140
 30 TTCTTTTTT TTTCTTTTT GCTACTGCAA ACGATGCTAT AATAAATGTC CTTATCAAAA 1200
 AAAAAAAAAA AAAAAAAAAA AAAAAANCCC NGGGGGGGGG CCCC GGGAAC NCAAT 1255

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(2) INFORMATION FOR SEQ ID NO: 76:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GGCACGAGAG AAATGTTTGA TTCTCTTTCC TATTTTAAGG GATCTTCTCT CTTGTTGATG 60
 TTGAAACTTT ACCTTAGTGA AGATGTGTTT CAACATGCTG TTGTCCTTTA CCTGCATAAT 120
 50 CACAGCTATG CATCTATTCA AAGTGATGAT CTGTGGGATA GTTTTAATGA GGTCAAAAC 180
 CAAACACTAG ATGTAAAGAG AATGATGAAA ACCTGGACCC TGCAGAAAGG ATTTCTTTTA 240
 55 GTGACTGTTT AAAAGAAAGG AAAGGAACTT TTTATACAAC AAGAGAGATT CTTTTTAAAT 300
 ATGAAGCCTG AAATTCAGCC TTCAGATACA AGGTACATGC CCTCTTTCTT TTCATGCCAT 360
 60 CTCTTTTGCA CTCTCAGGTG GAAATATTTT GAAGTGTGTT ATAATCATAA GTTCTTGTA 420

AACCTAACAA GATTATCCCT TCCTAAGAAT ACTTAACCTT CCTACCAAAT TAAAA

475

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(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

15

TTCTCTCTGC TCTTCGACTG CACCGCACTC GCGCGTGACC CTGACTCCCC CTAGTCAGCT 60
CAGCGGTGCT GCCATGGCGT GCGCGCGCGC CGAACCRGCG TCGGGGCTCG CGGCGTGTG 120
20 GCTCTGGCGT TGCTCGCCCT GGCCTGTGTC GTGCCCCGGG CCCGGGGCCG GGCTCTCGAG 180
TGGTTCTCGG CCGTGGTAAA CATCGAGTAC GTGGACCCGC AGACCAACCT GACGGTGTGG 240
AGCGTCTCGG AGAGTGGCCG CTTGCGCGAC AGCTCGCCCA AGGAGGGCGC GCATGGCCTG 300
25 GTGGGCGTCC CGTGGGCGCC CGGCGGAGAM CTCGARGGCT KCGCGCCCGA CACGCGCTTC 360
TTCGTGCCCG AGCCCGGCGG CCGAGGGGCC GCGCCCTGGG TCGCCCTGGT GGTGCTGGGG 420
30 GCTGCACCTT TCAAGGACAA AGTGCTGGTG GCGCGCGNGA ANGAA 465

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(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

45

ACATGCAGCC CAACTACAGA TTCTTATGGA ATTCTCAAG GTTGCAAGAA GAAATAAGAG 60
AGAGCAACTG GAACAGATCC AGAAGGAGCT AAGTGTTTTC GAAGAGGATA TTAAGAGAGT 120
GGAAGAAATG AGTGGCTTAT ACTCTCCTGT CAGTGAGGAT AGCACAGTGC CTCAATTGTA 180
50 AGCTCCTTCT CCATCACACA GTAGTATTAT TGATTCCACA GAATACAGCC AACCTCCAGG 240
TTTCAGTGGC AGTTCCTAGA CAAAGAAACA GCCTTGGTAT AATAGCACGT TAGCATCAAG 300
ACGAAAACGA CTTACTGCTC ATTTTGAAGA CTTGGAGCAG TGTTACTTTT CTACAAGGAT 360
GTCTCGTATC TCAGATGACA GTCGAACTGC AAGCCAGTTG GATGAATTTT AGGAATGCTT 420
GTCCAAGTTT ACTCGATATA ATTCAGTACG ACCTTTAGCC ACATTGTCAT ATGCTAGTGA 480

60

	TCTCTATAAT GGTTCAGTA TAGTCTCTAG TATTGAATTT GACCGGGATT GTGACTATTT	540
	TGCGATTGCT GGAGTTACAA AGAAGATTAA AGTCTATGAA TATGACACTG TCATCCAGGA	600
5	TGCAGTGGAT ATTCATTACC CTGAGAATGA AATGACCTGC AATTCGAAAA TCAGCTGTAT	660
	CAGTTGGAGT AGTTACCATA AGAACCTGTT AGCTAGCAGT GATTATGAAG GCACTGTTAT	720
10	TTTATGGGAT GGATTACAG GACAGAGGTC AAAGGTCTAT CAGGAGCATG AGAAGAGGTG	780
	TTGGAGTGTT GACTTTAATT TGATGGATCC TAAACTCTTG GCTTCAGGTT CTGATGATGC	840
	AAAAGTGAAG CTGTGGTCTA CCAATCTAGA CAACTCAGTG GCAAGCATTG AGGCAAAGGC	900
15	TAATGTGTGC TGTGTTAAAT TCAGCCCTC TTCCAGATAC CATTTGGCTT TCGGCTGTGC	960
	AGATCACTGT GTCCACTACT ATGATCTTCG TAACACTAAA CAGCCAATCA TGGTATTCAA	1020
20	AGGACACCGT AAAGCAGTCT CTTATGCAAA GTTGTGAGT GGTGAGGAAA TTGTCTCTGC	1080
	CTCAACAGAC AGTCAGCTAA AACTGTGGAA TGTAGGGAAA CCATACTGCC TACGTTCTTT	1140
	CAAGGGTCAT ATCAATGAAA AAAACTTTGT AGGCCCTGGCT TCCAATGGAG ATTATATAGC	1200
25	TTGTGGAAGT GAAAATAACT CTCTCTACCT GTACTATAAA GGACTTTCTA AGACTTTGCT	1260
	AACTTTTAAG TTTGATACAG TCAAAAGTGT TCTCGACAAA GACCGAAAAG AAGATGATAC	1320
30	AAATGAATTT GTTAGTGCTG TGTGCTGGAG GGCCTACCA GATGGGGAGT CCAATGTGCT	1380
	GATTGCTGCT AACAGTCAGG GTACAATTAA GGTGCTAGAA TTGGTATGAA GGGTTAACTC	1440
	AAGTCAAATT GTACTTGATC CTGCTGAAAT ACATCTGCAG CTGACAATGA GAGAAGAAAC	1500
35	AGAAAATGTC ATGTGATGTC TCTCCCCAAA GTCATCATGG GTTTTGGATT TGTTTTGAAT	1560
	ATTTTTTCT TTTTTCTTT TCCCTCCTTT ATGACCTTTG GGACATTGGG AATACCCAGC	1620
40	CAACTCTCCA CCATCAATGT AACTCCATGG ACATGCTGCT TCTTGGTGGT GTTATCTAAT	1680
	TTTGTGATA GGGAAACAAA TTCTTTTGAA TAAAAATAAA TAACAAAACA ATAAAAGTTT	1740
	ATTGAGCCAC AGTTGAGCTT GGAAAGTTTT TGTCAAATGC NGCAAGAGAT AACTCTTTTT	1800
45	ANGAAGTAGC ATATGTGAAC TATAATGTAA CAGTGAATAA TTTGTAAAGT TCGTATTTCC	1860
	CAACCTCTTT GGGAATTACA CATATCAATA TAAACAAAAT ATAAAGT	1907

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(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

GCTGGGGTGT CCCCKCSGCC ACCATCGTCA TCGCTTACTT GATGAAGCAC ACTCGGATGA 60
 CCCATGACTG ATGCTTATAA ATTTGTCAAA GGCAAACGAC CAATTATCTC CCCAAACCTT 120
 5 AACTTCATGG GGCAGTTGCT AGAGTTCGAG GAAGACCTAA ACAACGGTGT GACACCGAGA 180
 ATCCTTACAC CAAAGCTGAT GGGCGTGGAG ACGGTTGTGT GACAATGGTC TGGATGGAAA 240
 10 GGATTGCTGC TCTCCATTAG GAGACAATGA GGAAGGAGGA TGGATTCTGG TTTTMTTCT 300
 TTCTTTTCTT TTTTGTAGTT GGGAGTAAGT TTGTGAATGG AAACAACTT GTTTAAACAC 360
 TTTATTTTAA ACAAGTGTA GAAGACTATA ACTTTTGATG CCATTGAGAT TCACCTCCCA 420
 15 CAAACTGACA AATTAAGGAG GTTAAAGAAG TAATTTTCTT AAGCCAACAA TAAAAATATA 480
 ATACAACTTG TTTCTCCCCC TTTTCTTTT AAGCTATTG TAGAGTTTAT GACTAAATAG 540
 20 TCTGTGCAGG TTCATAGACC GAAGATACTA CACACTTTAA ACCAATTAAA AAGAACCAAA 600
 AGTAAATAGA AAAGACATG AATCACCAAG GCCTGGGATC AACCTGGGCT GTCCACACAG 660
 AAAACAAAAA CCAACCAAAA CCAAGCCCTG TTGTGCTCAC TGGTGCAAAG AGAAGATCAG 720
 25 GGCAGCTTAA GTGGTCTAAG RATCCTTCAG GCATTCTTTA AGGAGAAAAA GGATACCTTT 780
 GATTTTGTGT GTTTCATGCT CTGGATTTT TTTTMTTCT CTTCTCTGGG TTTAAGAGAT 840
 30 TTTTMTTGAA ATAGTGAGGA ACTGACCATT ATATGCCTTC ACTGGCTTCT TGTGCAATAA 900
 TATGATGTTT TAAGTGTC AACAAGTTAG AGCTGGCAGC TGAATGATAG ACAAATAGTG 960
 CAAATTTGCC AGCTTGAGA TAGAAAGGAA TTCAACAATA TATCAAATAC TTTCTTCCC 1020
 35 ACCTTTTCCC TTTTMTTCT TTTTMTCTGA TTGATCTG GTTACAGTGC CATAAACCTT 1080
 GTTACATATG TATATCAGAA TGTAAGAAAA AAAAATTTAT TTAAAAATAT TTTTCGCAA 1140
 40 AAAAAAANNA AAAAATCTGA GGGGGGCC 1168

45 (2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

55 AGAAAATCAC ATCCTAACAA AGAAGTCTGT CTAAGACAGT ACATCTCTTG TTGAACTTGC 60
 ATCTTTCCAC AGGACTTTCT GTTTTATAGG ATGAGACTAT TCTCTGCTTC ATCAAGGAAA 120
 GAGAAATGTT CAGGGTTGTA GGGATGGCAC ACTTATTAGT TCTGCCTGTC TGAAAGGTTT 180

	CTGCAGGACA GTTGGTCAG AGCTGCAATT CTAGTCCAT GGTCTAATGC TTGAGTATCT	240
	CTTCTTTCCC TTTCTGTCT CAGGAATCAG CTGAGAATTC ATTCGATTGT CATGCCTCTA	300
5	GCCCCTACT GTGATTGTT GGTGCACTT TCATTGCTT TAGTTCTAGA ATCACCTGTT	360
	GACTCCTCAG ACTTCACCTA ACTTTGGAAA CTCTCTTTTG GAGGCTTCTC ATTTCCCCCT	420
10	AATTCTGTGC TGCCTGAGCC CTAGAATTTT CCCACCAACG AATTATTCCA GGTAGATCCT	480
	AAGTTGCTGG ATCTAGTTGA TATTTAAACA ATATCTAGTT GATATTCTC ATTCAGTTGG	540
	ATCCAGAAAC CAGTATCTCT NAAAAACAAC CTCTCATACC TTGTGGACCT AATTTTGTGT	600
15	GCGTGTGTGT GTGCGCGCAT ATGTATATAG ACAGGCACAT CTTTTTACT TTTGTAAAAG	660
	CTTATGCCTC TTTGGTATCT ATATCTGTGA AAGTTTAAAT GATCTGCCAT AATGTCTTGG	720
20	GGACCTTGT CTTCTGTGTA AATGGTACTA GAGAAAACAC CTATATTATG AGTCAATCTA	780
	GTTGGTTTTA TTCGACATGA AGGAAATTTT CAGATAACAA CACTAACAAA CTCTCCCTTG	840
	ACTAGGGGGA CAAAGAAAAG CAAACTGAC CATAAAAAAC AATTACCTGG TGAGAAGTTG	900
25	CATAAACAGA ATTAGGTAGT ATATTGAAGA CAGCATCATT AACAGTTAT GTTGTCTCTC	960
	TTGCAAAAAA CATGTACTGA CTTCCCGTTG AGTAATGCCA AGTGTTTTTT TTTATTATAA	1020
30	AACTTGCCCT TCATTACATG TTTCAAAGTG GTGTGGTGGG CCAAATATT GAAATGATGG	1080
	AACTGACTGA TAAAGCTGTA CAAATAAGCA GTGTGCCTAA CAAGCAACAC AGTAATGTTG	1140
	ACATGCTTAA TTCACAAATG CTAATTTTAT TATAAATTGT TTTGCTAAAA TACACTTTGA	1200
35	AACTATTTTT CTGTATTCCA AGAGCTGAGA TCTTAGATTT TATGTAGTAT TAAGTGAAAA	1260
	AATACGAAAA TAATAACAT TGAAG	1285

40

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

	TCTCCAGCCC CAATTTCTAC GCGCACCGGA AGACGGAGGT CCTCTTTCCT TGCCTAACGC	60
	AGCCATGGCT CGTGGTCCCA AGAAGCATCT GAAGCGGGTG GCAGCTCCAA AGCATTGGAT	120
55	GCTGGATAAA TTGACCGGTG TGTGTCTCC TCGTCCATCC ACCGGTCCCC ACAAGTTGAG	180
	AGAGTGTCTC CCCCTCATCA TTTTCTGAG GAACAGACTT AAGTATGCCC TGACAGGAGA	240
60	TGAAGTAAAG AAGATTTGCA TGCAGCGGTT CATTAAAATC GATGGCAAGG TCCGAAGTGA	300

TATAACCTAC CCTGCTGGAT TCATGGATGT CATCAGCATT GACAAGACGG GAGAGAATTT 360
 CCGTCTGATC TATGACACCA AGGGTCGCTT TGCTGTACAT CGTATTACAC CTGAGGAGGC 420
 5 CAAGTACAAG TTGTGCAAAG TGAGAAAGAT CTTTGTGGGC ACAAAGGAA TCCCTCATCT 480
 GGTGACTCAT GATGCCCGCA CCATCCGCTA CCCCATCCC CTCATCAAGG TGAATGATAC 540
 10 CATTTCAGATT GATTTCAGAGA CTGGCAAGAT TACTGATTTC ATCAAGTTCC ATTCACCCAG 600
 CCAGGTGGTC TCGTCACCTC AGAGGCTCCG CAGACTCCTG CCCAGGCCAG GACTGAGGCA 660
 AGCCTCAAGG CACTTCTAGG ACCTGCCTCT TCTACCAAG ATGAACTCAC TGGTTTCTTG 720
 15 GCAGCTACTG CTTTTCCTCT GTGCCACCCA CTTTGGGGAG CCATTAGAAA AGGTGGCCTC 780
 TGTGGGAAT TCTAGACCCA CAGGCCAGCA GCTAGAATCC CTGGGCCTCC TGGCCCCSGG 840
 20 GGAGCAGAGC CTGCCGTGCA CCGAGAGGAA GCCAGCTGCT ACTGCCAGGC TGAGCCGTCC 900
 GGGGACCTCG CTGTCCCCGC CCCCCGAGAG CTCCGGGAGC CCCAGCAGC CGGGCCTGTC 960
 CGCCCCCAC AGCCGCCAGA TCCCCGCACC CCAGGGCGCG GTGCTGGTGC AGCGGGAGAA 1020
 25 GGACCTGCCG AACTACAAC TGAACCTCTT CGGCCTGCGC TTCGGCAAGC GGGAGGCGGC 1080
 ACCAGGGAAC CACGGCAGAA GCGCTGGGCG GGGCTGAGGG CGCAGGTGCG GGGCAGTGAA 1140
 30 CTTTCAGACCC CAAAGGAGTC AGAGCATGCG GGGCGGGGCG GGGGGGCGGG GACGTAGGGC 1200
 TAAGGGAGGG GCGCTGGAG CTTCCAACCC GAGGCAATAA AAGAAATGTT GCGTAACTCA 1260
 AAAAAAAAAA AAAAAAANC TCGGGGGGGG 1290
 35

(2) INFORMATION FOR SEQ ID NO: 82:
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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 684 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TTTATGTAT TCTGTAACTA TAGAACTTCT ATTWATTCCT TTTTGGACT TGCTAAGTTG 60
 50 TCTTTWATGG TTTTWAGTTC CATGCTGAAG TTTTCAGTAT TGACTTATCC CCTTGAACAT 120
 GAGTTGTTTT ATAGACTCTR ATGATTCAAA AATCTTACAT CTTTGGTAG TCTCTTTCAT 180
 55 TTGTYCACTG TTTCTGTGTA TTTWACTCA TGGTATTTTA ATTCTTCGTT WTTTTTTTTC 240
 TGTTWAGAWA CATTCTTTGA AAAATAATTT GGAGGAATAT TTGATTTCTTA TGAACAAGGC 300
 ATTACTCACC AGAGAAGAT TTTTGTGTTT ACCARGTGCC TARGAATGCT AACAGTCTGG 360
 60

	GAMCACATAG AMCACCAGGT GATGAGACAA TCCTGGGART CCTGTMTTAC TTTGGSCCAT	420
	CTTTTCTCCC AACCTGTGG GAATARTCAT YCATATCCTA RCTGCAGGCT ARAAGGTGGT	480
5	TTATCAGAGC CCAACTTCGA GGGCTCTGGG CTTTAGCTAC TGTCAACCCA TCATAACTGA	540
	GCTTCATGGA TTGATTCTCT TTTTATCTTT CAGATTTTCT TTTAAAAATC TTTGTMTT	600
10	TTTTTCTTCC GAAAGATTCC CCCAACATTA CCATTCACCA CCTTCCGTG AATTTTTTTG	660
	GCTCTCATTT TGAATTTTTC AAGA	684
15	(2) INFORMATION FOR SEQ ID NO: 83:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 2024 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:	
	CTGCAGGAAT TCGGCACAGC TGCGCTGGAG GCTTCATCTT TGCCGCCGCT GCCGTCGCCT	60
	TCCTGGGATT GGAGTCTCGA GCTTCTCTCG TTCGTTCTGYC GCGGGGTTTC CGCCCTTCTC	120
30	GCGCCTCGGG GCTGCGAGGC TGGGAAGGG GTTGGAGGGG GCTGTTGATC GCCGCGTTTA	180
	AGTTGCGCTC GGGGCGGCCA TGTCGGCCGG CGAGGTCGAG CGCCTAGTGT CGGAGCTGAG	240
35	CGCCGGGACC CGAGGGGATG AGGAGGAAGA GTGGCTCTAT GCGGATGAAA ATGAAGTTGA	300
	AAGGCCAGAA GAAGAAAATG CCAAGTCTAA TCCTCCATCT GGAATTGAAG ATGAAACTGC	360
	TGAAAATGGT GTACCAAAAC CGAAAGTGAC TGAGACCGAA GATGATAGTG ATAGTGACAG	420
40	CGATGATGAT GAAGATGATG TTCATGTCAC TATAGGAGAC ATTAAAACGG GAGCACCACA	480
	GTATGGGAGT TATGGTACAG CACCTGTAAA TCTTAACATC AAGACAGGGG GAAGAGTTTA	540
45	TGGAATACA GGGACAAAAG TCAAAGGAGT AGACCTTGAT GCACCTGGAA GCATTAATGG	600
	AGTTCCACTC TTAGAGGTAG ATTTGGATTC TTTTGAAGAT AAACCATGGC GTAAACCTGG	660
	TGCTGATCTT TCTGATTATT TTAATTATGG GTTTAATGAA GATACCTGGA AAGCTTACTG	720
50	TGAAAAACAA AAGAGGATAC GAATGGGACT TGAAGTTATA CCAGTAACCT CTACTACAAA	780
	TAAAATTACG GTACAGCAGG GAAGAACTGG AACTCAGAG AAAGAACTG CCCTTCCATC	840
55	TACAAAAGCT GAGTTTACTT CTCCTCCTTC TTTGTCAAG ACTGGGCTTC CACCGAGCAG	900
	GAGATTACCT GGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG	960
	CAGGCGACGG GCAAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA	1020
60	AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTCCCT CCAGGAGCTC CTCCCACTCA	1080

CCTTCCACCT CCTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT 1140
 TCCACCACCG GGTTTTCCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT 1200
 5 AGAAAGTGA CATTCCTCTG GTTATGATAG TCGTTCTGCA CGTGCATTTC CATATGGCAA 1260
 TGTTCCTTTT CCCCATCTTC CTGGTTCTGC TCTTTCGTGG CCTAGTCTTG TGGACACCAG 1320
 10 CAAGCAGTGG GACTATTATG CCAGAAGAGA GAAAGACCGA GATAGAGAGA GAGACAGAGA 1380
 CAGAGAGCGA GACCGTGATC GGGACAGAGA AAGAGAACGC ACCAGAGAGA GAGAGAGGGA 1440
 GCGTGATCAC AGTCTACAC CAAGTGTMTT CAACAGCGAT GAAGAACGAT ACAGATACAG 1500
 15 GGAATATGCA GAAAGAGGTT ATGAGCGTCA CAGAGCAAGT CGAGAAAAAG AAGAACGACA 1560
 TAGAGAAAGA CGACACAGGG AGAAAGAGGA AACCAGACAT AAGTCTTCTC GAAGTAATAG 1620
 20 TAGACGTCGC CATGAAAGTG AAGAAGGAGA TAGTCACAGG AGACACAAAC ACAAAAAATC 1680
 TAAAAGAAGC AAAGAAGGAA AAGAAGCGGG CAGTGAGCCT GCCCCTGAAC AGGAGAGCAC 1740
 CGAAGCTACA CCTGCAGAAT AGGCATGGTT TTGGCCTTTT GTGTATATTA GTACCAGAAG 1800
 25 TAGATACTAT AAATCTGTGTT ATTTTCTGG ATAATGTTTA AGAAATTTAC CTTAAATCTT 1860
 GTTCTGTTTG TTAGTATGAA AAGTTAACTT TTTTCCAAA ATAAAGAGT GAATTTTCA 1920
 30 TGTTAAGTTA AAAATCTTTG TCTGTACTA TTTCAAAAAT AAAAAGACAG CAATGACTTT 1980
 ATATCCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC GGCC 2024

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(2) INFORMATION FOR SEQ ID NO: 84:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 931 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CGCGCCMATA GCCGGACGGG GATCTGAGCT GGCAGGATGA ATGTGGGGGT GGCACACAGC 60
 GAAGTAAACC CCAACACCCG AGTGATGAAT AGCCGAGGCA TCTGGCTGGC CTACATCATC 120
 50 TTGGTAGGAT TGCTGCATAT GGTCTACTC AGCATCCCCT TCTTCAGCAT TCCTGTTGTC 180
 TGGACCTGA CCAACGTCAT CCATAACCTG GCTACGTATG TCTTCCTTCA TACGGTGAAA 240
 55 GGGACACCCT TTGAGACTCC TGACCAAGGA AAGGCTCGGC TACTGACACA CTGGGAGCAA 300
 ATGGAATATG GGCTCCAGTT TACCTCTTCC CGCAAGTTCC TCAGCATCTC TCCTATTGTG 360
 CTCTATCTCC TGGCCAGCTT CTATACCAAG TATGATGCTG CGCACTTCCT CATCAACACA 420
 60

GCCTCATTGC TAAGTGTACT GCTGCCGAAG TTGCCCCAGT TCCATGGGGT TCGTGTCTTT 480
 GGCATCAACA AATACTGAGG GATGGGTTTT GGGACAGCTC CATGGGCATG GGAAGGCAC 540
 5 TGAAACAGAG GACTATAAAA CATCCTTCTC TTATTCTCCA TACTGTCTTC TACACCTTTA 600
 AAGCCTGAGA ACTATACAAC CTTTCCCAGA CTCCAAGAA GAGAAGAGAT TGGCAAATGG 660
 GGCTCCTGGG CCCAGTCTG CTAGTGGCAA GTTCTTTGA ATCAGGAAGG CAGGTGAGGT 720
 10 AAGGGCCAAA TCACTCTCCT CCATAGCAGG AAGCCATTG GGCAGCTCCT TTGGTGATTA 780
 CATCTTTCCA TATCTTTTAC ACTTACCACC TTCCAGCTCT GTTTTGCTGT GTATTTTCT 840
 15 TACAATAATT TTTTTCAGCT ATAGCTGCAG TTAAATCAGG ATGGGTAGAG AGCTGTCTCT 900
 ATAAGGCTGG GGGTGGGAAG ATGAATACT G 931

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(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 825 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CGGGGCCGGC GGGGTCTTCA GGTACCGGG CTGTTACAG CAGCTCTACC CCTCACGACG 60
 CAAACATGGC AGCGCAGAAG GACCAGCAGA AAGATGCCGA GCGGAAGGG CTGAGCGGCA 120
 35 CGACCCTGCT GCCGAAGCTG ATTCCCTCCG GTGCAGGCCG GGAGTGGCTG GAGCGGCGCC 180
 GCGCGACCAT CCGGCCCTGG AGCACCTTCG TGGACCAGCA GCGCTTCTCA CGGCCCCGCA 240
 40 ACCTGGGAGA GCTGTGCCAG CGCCTCGTAC GCAACGTGGA GTACTACCAG AGCAACTATG 300
 TGTTCGTGTT CCTGGGCCTC ATCCTGTACT GTGTGGTGAC GTCCCTATG TTGCTGGTGG 360
 CTCTGGCTGT CTTTTTCGGC GCCTGTACA TTCTCTATCT GCGCACCTTG GAGTCCAAGC 420
 45 TTGTGCTCTT TGGCCGAGAG GTGAGCCCAG CGCATCAGTA TGCTCTGGCT GGAGGCATCT 480
 CCTTCCCCTT CTTCTGGCTG GCTGGTGCGG GCTCGGCCGT CTTCTGGGTG CTGGGAGCCA 540
 50 CCCTGGTGGT CATCGGCTCC CACGCTGCCT TCCACCAGAT TGAGGCTGTG GACGGGGAGG 600
 AGCTGCAGAT GGAACCGTG TGAGGTGTCT TCTGGGACCT GCCGGCCTCC CGGGCCAGCT 660
 GCCCCACCCC TGCCCATGCC TGTCTGCAC GGCTCTGCTG CTCGGGCCCA CAGCCCGCTC 720
 55 CCATCACAAG CCCGGGGAGG GATCCCGCCT TTGAAAATAA AGCTGTTATG GGTGTCATTC 780
 AGGAAAAAAA AAAAAAAGG GGGGCCCTC TAGGGGTCAA AGTTA 825

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(2) INFORMATION FOR SEQ ID NO: 86:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CATGTAAAAG GATGAAATGT GACTTCTGGT GTTTTTTTAT TTCTATGGAG GGACTTTCTG 60

15 GGGACGGTTT CTGGCTCTCA GGCTCTGAGA AGCTGCAGTT TATGAGTGGC TCTGTGTGTG 120

CTGCCACCTA CTGGAGAAGC CATAAGCTGC AGCTTTAGGA AAAGGGAACC CGGGGCAGAG 180

TGTGGGGAAG TGGGATGGCA GCATGGCAGG GCTTTGAAA ATGAGAGGTG AGAGTKTKTC 240

20 CAGGAAGGGT GTAAGGAGAG GATGGATCCT GATACATGGA TTCAGGATCA TTAGGGTCCT 300

GTCTGGGACA CTGGCCTTCC TGCTTACCTG CTCTTTCCTT CCTCCTTGGT CGGAGGAGGG 360

25 GCTGGCTCAC TGCTCTGGCT TCATTTTCCA GAGCTGCCTG CTGCAGTCAC ACTTAGGTCA 420

TCTTCTCTCA CTTTTCTCCT TTTGCCGATT AGTGGACGTG ACAGAGATGT GAATGGGGCA 480

GGGATGTCCT TTGATGGCAT CAAGACTTTA GCTTCTGGTG CGCTGTGTCC CAGCTCTGAT 540

30 TTCAGTTGCA GCCGTGATGG AMAGTTNGCA TGGAAGCTGA GACTCTCACT GACAGTGAAA 600

CCCTCAAATG AACACAATCC CTGCTTTCCT GCCAAGGATC CTTGTAGGGT NCCCCAGCT 660

35 TCCCCACTTT TTTTCTGTGT CCTGACAAAG AAACACAGAG TAACTTGATT GCCCTGTGAC 720

CTGGCCAGTT GCATTTCCCC TGCAGGCTTG AGCCCAAGCC AGAGCCTTGA AAAGGTATTC 780

AGGTTGTTGC CCAAAACACT GAAAAAACT GCCCTGGCCC TGAACCAAAT ACCTTGAACC 840

40 CTCGTAAACT CCATACCCTG ACCCCCTTGT TTTGGATATA CCCAGGTAGA ACAACTCTCT 900

CTCACTGTCT GTTGTGAGGA TACGCTGTAG CCCACTCATT AAGTACATTC TCCTAATAAA 960

45 TGCTTTGGAC TGATCACCCCT GCCAGTCTTT TGTCTTGGGC AATCTATACT TTTNCTCAGA 1020

GGTTCCCAAG GCCTACTGAA GGGACTTAAC ATACTCTTAA TGGCTTTCCT CTCTCTTGTT 1080

TTACCTTATG CCCTCACTTC CTGAGTTAAC CTCCCAAATA CAGGATTCAC CTGTACCCAA 1140

50 GCCCTTAGCT TCAAGAATAC AGGATCACCT GTACCCAAGC CCTTAGCTCA AGCTCTGCTT 1200

TGGAAGAACC CAACTAAGA CAGTGCTCCT GGTGCCCT 1238

55

(2) INFORMATION FOR SEQ ID NO: 87:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

	ATTGCCTTCT GGTCCCTGGT GACACTGGGG TCATCCTTCA TCCCGGAGA GCATTTCTGG	60
10	CTGCTCCTCC TGACCCGGGG CCTGGTGGGG GTCGGGAGG CCAGTTATTC CACCATCGCG	120
	CCCCTCTCA TTGCCGACCT CTTGTGGCC GACCAGCGG ACCGGATGCT CAGCATCTTC	180
15	TACTTTGCCA TTCCGGTGGG CAGTGGTCTG GGCTACATTG CAGGCTCCAA AGTGAAGGAT	240
	ATGGCTGGAG ACTGGCACTG GGCTCTGAGG GTGACACCGG GTCTAGGAGT GGTGGCCGTT	300
	CTGCTGCTGT TCCTGGTAGT GCGGGAGCCG CCAAGGGGAG CCGTGGAGCG CCACTCAGAT	360
20	TTGCCACCCC TGAACCCAC CTCGTGGTGG GCAGATCTGA GGGCTCTGGC AAGAAATCCT	420
	AGTTTCGTCC TGTCTTCCT GGGCTTCACT GCTGTGGCCT TTGTCACGGG CTCCTGGCT	480
25	CTGTGGGCTC CGCATTCCT GCTGCGTTC CGCGTGGTCC TTGGGGAGAC CCCACCCTGC	540
	CTTCCCGGAG ACTCCTGCTC TTCCTCTGAC AGTCTCATCT TTGGAATCAT CACCTGCCTG	600
	ACCGGAGTCC TGGGTGTGGG CCTGGGTGTG GAGATCAGCC GCCGGCTCCG CCACTCCAAC	660
30	CCCCGGGCTG ATCCCTGGT CTGTGCCACT GGCCTCCTGG GCTCTGCACC CTTCCTCTTC	720
	CTGTCCCTTG CTTGCGCCCG TGGTAGCATC GTGGCCACTT ATATTTTCAT CTTCAATGGA	780
35	GAGACCCTCC TGTCCATGAA CTGGGCCATC GTGGCCGACA TTCTGCTGTA CGTGGTGATC	840
	CCTACCCGAC GCTCCACCGC CGAGGCCCTC CAGATCGTGC TGTCCACCT GCTGGGTGAT	900
	GCTGGGAGCC CTTACCTCAT TGGCCTGATC TCTGACCGCC TGCGCCGAA CTGGCCCCC	960
40	TCCTTCTTGT CCGAGTTCCG GGCTCTGCAG TTCTCGCTCA TGCTCTGCCG GTTTGTGGG	1020
	GCACTGGGCG GCGCACTTCC TGGGCACCGC CATCTTCATT GAGGCCGACC GCCGCGGGC	1080
45	ACAGCTGCAC GTGCAGGGCC TGCTGCACGA AGCAGGGTCC ACAGACGACC GGATTGTGGT	1140
	GCCCCAGCGG GGCCGCTCCA CCCGCGTGCC CGTGGCCAGT GTGCTCATCT GGAGAGGCTG	1200
	CCGCTCACCT ACCTGCACAT CTGCCACAGC TGCCCTGGG CCCACCCAC GAAGGGCCTG	1260
50	GGCCTAAACC CCTTGGCCTG GCCCAGCTTC CAGAGGGACC CTGGGCCGTG TGCCAGCTCC	1320
	CAGACACTAC ATGGGTAGCT CAGGGGAGGA GGTGGGGGTC CAGGAGGGG ATCCCTCTCC	1380
55	AACAGGGGCA GCCCAAGGG CTCGGTGCTA TTTGTAACGG GATTAAAATT TGTAGCCAGA	1440
	AAAAAAAAA AAAAAAAAAA	1460

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(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

10 CAGGTGCAAA GTGGGAAGTG TGAGTCCTCA GTCTTGGGCT ATTCGGCCAC GTGCCTGCCG 60
GACATGGGAC GCTGGAGGGT CAGCAGCGTG GAGTCTGGC CTTTTCGCTC CACGGGTGGG 120
15 AAATTGGCCA TTGCCACGGC GGAAGCTGGG ACTCAGGCTG CCCCCCGGCC GTTCTCATC 180
CGTCCACCGG AYTCTGGGC GCTCGCACTG GCGCTGATGT AGTTTCTGA CCTCTGACCC 240
GTATTGTCTC CAGATTAAAG GTACGACATT TGGAGGCCCC AGCGAGAAAC GTCACCGGGA 300
20 GAAACGTCAC CGGGCGAGAG CGGKCCCGCT GTGTGCTCCC CCGGAAGGAC AGCCAGCTTG 360
TAGGGGGGAG TGCCACCTGA AAAAAAATT TCCAGGTCCC CAAAGGGTGA CCGTCTTCCG 420
25 GAGACAGCGG ATCGACTACC ATGTGGGTGC CCACAAAAT TYCACCTYTG AGTCTCAAC 480
TGCTGACCCC GGGTCACTT CCAGAGAGAA GGAATCCCTC CTGCTTGGAA GAGACCTCAC 540
ACCGTCATCA CGATGCCAAC GGCTCTGAAG GTGGATGGCA TTCTGCGTG GATTCATCAC 600
30 TCCCGCATCA AAAAGGCCAA CRGAGCCCA CTAGAAACAT GGGTCCCCAG GGCTGGGTCA 660
GGCCCCTTAA AACTGCACCT AAGTTGGGTG AAGCCATTAG ATTAATCTT TTTCTTAATT 720
35 TTGTAAACA ATGCATAGCT TCTGTCAACT TATGTATCTT AAGACTCAAT ATAACCCCT 780
TGTTATAACT GAGGGAATCA ATGATTTGAT TCCCCAAAA CACAAGTGGG GAATGTAGTG 840
TCCAACCTGG TTTTACTAA CCTGTCTTTT AGACTYTCCC TTCTCTTTAA TCACTCAGCC 900
40 TTGTTCCAC CTGAATTGAC TCTCCCTTAG CTAAGAGCGC CAGATGGACT CCATCTTGGC 960
TCTTCTNACT GGCAGCCGCT TCTYCAAGG ACTTAACTTG TGCAAGCTGA CTCCAGCAC 1020
45 ATCCAAGAAT GCAATTAACT GATAAGATAC TGTGGCAAGC TATATCCGA GTTCCCAGGA 1080
ATTCGTCCAA TTGATTACAC CMAAAGCCC CGCGTCTATC ACCTTGTAAT AATCTTAAAG 1140
CCCCTGACC TGGAATATT AACGTCTCTG TAACCATTTA TCCTTTTAACT TTTTTCCT 1200
50 ACTTTATTTT TGTAATTTG TTTTAACTAG ACCCCCCCTC TCCTTTCTAA ACCAAAGTAT 1260
AAAAGCAAAT CTAGCCCTT CTTAGGCGG AGAGAATTTC GAGCGTTAGC CGTCTCTTGG 1320
55 CCACCAGCTA AATAACGGA TTCTTCATGT GTAAAAAAA AAAAAAAA CTCGGAGGGG 1380
GGGCCCCGTA CCAA 1395

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GGCACGAGCC GGCAAGCCGA GCTAGGGTGA AAAGTGGGG CGCACCAGGA TGTNNGACAG 60
AAAAGCAGAA GATGAGACTC TGTTCATTCA CTTTTCCTAG GCCCATCCTG TGGTCATCTT 120
15 TCCCCCTCCC ATCATACCTC CTCCTTCCTG GAGCCTCTGC CGGCTTGGCT GTAATGGTGG 180
CACTTACCTG GATATTTTCA TGGGAGGATG AAAGGCGAGA CTCACCCTAC GCGGTGGGAC 240
20 AGATGGGGAG AGGAAAAAGG CAGAGATGGC CAGGAGAGGG GTGCAGGACA AACCAGAGAG 300
GTTGGGTCAG GGGAAAAGGG TGGGGAGAAA GAGGGGTGCA GGCCCTGCAG GCCGGTTAGC 360
CAGCAGCTGC GGCCTCCCCG GGCCCTTGGC ATCCAACCTC GCAGACAGGG TACCAGCCTC 420
25 CTGGTGTGTA TCATAGGATT TGTTCACATA GTGTTATGCA TGATCTTCGT AAGGTTAAGA 480
AGCCGTGGTG GTGCACCATG ACATCCAACC CGTATATATA AAGATAAATA TATATATATA 540
30 TGTATGTAAA TTATGGCAG AGAAATTATA GCACTGAGGG CCCTGCTGCC CTGCTGGACC 600
AAGCAAACT AAGCCTTTTG GTTTGGGTAT TATGTTTCGT TTTGTTATTT GTTTGTTTTT 660
GTGGCTTGTC TTATGTCGTG ATAGCACAAG TGCCAGTCGG ATTGCTCTGT ATTACAGAAT 720
35 AGTGTTTTTA ATTCATCAAT GTTCTAGTTA ATGCTACCT CAGCACCTCC TCTTAGCCTA 780
ATTTTAGGAG GTTGCCCAAT TTTGTTTCTT CAATTTTACT GGTACTTTT TTGTACAAAT 840
40 CAATCTCTTT CTCTCTTTCT CTCCTCCCCA CCTCTCACC TTGCCCTCTC CATCTCCCTC 900
TCCCGCCCTC CCCTCCTCCC TCTGGCTCCC CGTCTCATTT CTGTCCACTC CATTCTCTCT 960
CCCTCTCTCC TGCCTCCTGC TGCCCCCTCC CCAGCCCACT TCCCCGAGTT GTGCTTGCGG 1020
45 CTCCTTATCT GTTCTAGTTC CGAAGCAGTT TCACTCGAAG TTGTGCAGTC CTGGTTGCAG 1080
CTTCCGCAT CTGCCTTCGT TTCGTGTAGA TTGACGCGTT TCTTTGTAAT TTCAGTGTTT 1140
50 CTGACAAGAT TTAAAAAAA AAAAAGGAAA AAAAAAATA AAAAAA 1186

55 (2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1821 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

5	AAAACATGCT TTCAGGGCGT CCCCTATGTA TTCGGGGGGC CCACGGACAC TCAGGCTGGA	60
	KATCCGTCCT CACTGCGCTC AAGATGGCCT CAGCAGACAC CAGTTACCCA GCTGAAAGTC	120
	ACAATCCCTC CCAGAAGTCT CCCAACACTA GTGCTGACCA GAGGTGGGGC TCTCAGGCTA	180
10	GGAGTTTCAC ACACAATGAC AGGCTGCTGG GGGACATTGC AGGACCCCTT TTCCTYTCCT	240
	CTCCATGCTA GAAGCCAGCC CTAGGMAGCT GCAGTTACTC CCTGTGACTC AGCAGCAGGC	300
15	TGATTCAACA CAGCTGCCCA CACAAAGCCA GTGGTAATAC ATCTGTTTAC CTTTCCCTAT	360
	CACCCAGACA CAAGCCCTT TCCCAGGTCA AACCACAGGC CGATGCATCT CCAGTTTGAC	420
	AGTCAAATCA CTACTTCCAT TGCTACTTTA GATCAGCCAA AGTGGTGACT GCTGCAGTGT	480
20	GTGGCTATCC CTACAAGGCC CACCCAAGGG ATGCCCAAAG CCCAACCTTC TCCAGGGCTG	540
	CAGCAGNAGC AACCCACCA GCCTAAGTCC AGCAGAGGAC CTCCCACCCA ATGCTCTGTT	600
25	CTAATTAGAA GGGGAAGTGA GCCACAGAAA ATCAACTTAT CTATAATTAC AAAATTCTCT	660
	TGACTCACCT TAAAGTTCCT ATTGACATCT ACTGCTTTTA AACCTATTTG AAAACTCTGA	720
	TACTAAAACA AATGACACTC TAAGAAAGTT TGGGAGCCCC ATGCTGAGAA CCATTTCTGT	780
30	GCAGTGAGGA TGTTTCCAGA AGCTACTTAC CTACATGTGA ATGTGCCATT TTCTTTCTCT	840
	TTGTAGAGAA AATCCCTTTT ACTTTTGGGA ACAGTAATGG CAGCTTCTAG TACAGCCATT	900
35	ACAGTTTCAT ATGAGAAAAA TTAAGAATAA CTATAAAATT GTTAAATAT CCAATAATGG	960
	ATAATGATGG CCAGAAGATT TAACATACAA AGTAATCTC AATGTAAAGC TATTCAGCTC	1020
	TTCCAGGTTG AATGCCCTGT AACCCACCCT GACCTTCCAC ATCATCTTCA AAAAGCAGTT	1080
40	TCTCTGTTCC CCATGATTCT CCTATAAGGT AACTCTTTAG TCCTCCATTT AGCACATTTT	1140
	AAATCCTCCA AAGAATAAGT ATCATGTGAT TATTTTAGCT TTACAAAAAA AAAGTTGAAT	1200
45	GGCGTTTTAT TTTCATGGCC TATAAGCAGG TACCTTAGTA GGCAGATAT AGGAAAAACA	1260
	AATTAGAGCA AAACAAATCC TCTACAAATC CAAGGCAGGA AAAGTGGTGG CAGAGTGACT	1320
	CATCTCTCTG TCCCTCCCAT CAGGTCAAAT CAGGAGGCTG CAGTGAATGC CTGTTCTTTG	1380
50	AATGTGTAGC AGTGTTCCT GTAACCTTTT AAAACTTGGC TATAGGCTGT TTAGCACAGT	1440
	ACAGATTAAA GATACAGTTA CGTAAACAGC AAAGTAATTT TATAGTGCTT CATCCATTTA	1500
55	TCATGCTTTG GTTTGCTAAT TTTTTCACAT ACCTTTTCT ATCACAGTCT GTTGCTTTTG	1560
	TACACATTTT TCATATTTGG GTTCGACAGG TAAACACAAA CTGCTATTTT AGTAGAAAAA	1620
60	GTTATTGTTA TGGAAATATTA AACCCAATAA ATGTATATAA GGGTAAAAAA AAAAAAAAAA	1680

AAAAAAAAA AAAAAAAAAA AAAAAAATTC CTGCGGGCCG CANGCTTTTT CCCTTTGGGT 1740
 GAGGGGTAT TTTNGGCTTG GGCACGGGC CCTTCGTTTT TACAACGTCG TGANGGGGGG 1800
 5 AACCCGGGGG GGGTTTCCCC C 1821

10 (2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

20 TGCCCTTTTT CCCACCGATT CGGGGNTGG TGAAGGTGGG AGATGTGAAC TCCAATTAAG 60
 GGACTGGAGA GAGGTGAAGA ATTTTGCAGG TGGGAGATTG GGATTTGAAT GTGGACTTGT 120
 25 AAATGACTTG ACCTTGCCAT CTGTGTTCAA GGTACGGTT TGCTGTGGGG TTCTGGGAG 180
 AGCTTACTCA CCCCGGAGTC TTTTCTTTCT CTGCTCCAA GAAGAGCCCT GTTGGTGCTT 240
 TACCACCGCT TGGAGTCTCC CGAGGACACA AACAGGCAGA GAGGGACGTG TAGGGAGAGT 300
 30 TCTTTCCTGT TTTCTGTGCT TTCCTTTTTA CAGGACTCCC GGAAGGCCAC TCATGGCCAT 360
 GCCAGGAGCT TTCTCAGAAA CAGTCATAAA CGATCTCTTG AGTCTCTTTC TTGTCTCTCC 420
 35 AGCTGAGCTT TCTATTCCA CCTTTCTGG TGTCTATAGG AATGCATGAG AAGACCCTGG 480
 GACGTTTTTC TGCTCTCTTC TGGCCCTCCA TGGAGCCATG GGCCTCGGCC TCGGCGGCTC 540
 CTCACCTCA CAATTTATTT CCTCCTCCCG TGCCAGCCCT TCTTTTGTGT CTGAAACCGG 600
 40 TTTTAAATG TGA CTCTCCC AGAGAAGAAG CCGCTGGCTG TATGAAACTT GACGGCGCTT 660
 TTGTAAGGTG CCACCCCAA ACTTTAAGGT AGCTAAACCA ATTTTAAAA GATTCAATGG 720
 45 CTGTTCATC CTCCAGATGT AGCTATTGAT GTACACTCG CAACGGAGTG TCTGAAATTG 780
 TGGTGGTCTT GATTTATAGG ATTTTATAAT TAAAATGTCT GCTGAATAAA AAAAAAAAAA 840
 AAAA ACTCGA GGGGGGCCCC GT 862

50

(2) INFORMATION FOR SEQ ID NO: 92:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 696 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

	CTGAGGCGAG TGAAGTGGAC TCTGAGGGCT ACCGCTACCG CCACTGCTGC GGCAGGGGCG	60
5	TGGAGGGCAG AGGGCCCGCG AGGCCGCGT TGCAAACATG GCTCAGAGCA GAGACGGCGG	120
	AAACCCGTTT GCCGAGCCCA GCGAGCTTGA CAACCCCTTT CAGGACCCAG CTGTGATCCA	180
10	GCACCGACCC AGCCGGCAGT ATGCCACGCT TGACGTCTAC AACCCCTTTG AGACCCGGGA	240
	GCCACCACCA GCCTATGAGC CTCCAGCCCC TGCCCCATTG CCTCCACCCT CAGCTCCCTC	300
	CTTGACGCCC TCGAGAAAGC TCAGCCCCAC AGAACCTAAG AACTATGGCT CATAACGAC	360
15	TCAGGCCTCA GCTGCAGCAG CCACAGCTGA GCTGCTGAAG AACAGGAGG AGCTCAACCG	420
	GAAGGCAGAG GAGTTGGACC GAAGGAGCGA GAGCTGCAGC ATGCTGCCCT GGGRGGCACA	480
20	GCTACTCGAC AGAACAATTG GCCCCCTCTA CCTTCTTTT GTCCAGTTCA GCCCTGCTTT	540
	TTCCAGGACA TCTCCATGGA GATCCCCCAA GAATTTTACA AGACTGTATC CACCATGTAC	600
	TACCTCTGGA TGTGCAGCAC GSTGGNTCTT CTCTGAAYT TCMTGGSCTG CCTGGCCAGT	660
25	TCTGTGTGGA AACCAACAAT GCGAGGGCTT TGGGTT	696

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|-----------------------------|
| | (A) LENGTH: 1886 base pairs |
| 35 | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

40	CAGGCCACTG ACGCTTCTTT GCGAGGGATG CAGGAGGTCC TACAGAGAAA GCGCTTCTT	60
	GCATKTCAGA GGGCCACAG CCTGTCACCC ACAGATCACC AAGCAGCTTT CTACCTGGCT	120
45	CTGCAGCTTG CCATCTCCAG ACAGATCCCA GAGGCTCTGG GGTATGTCCG CCAAGCTCTT	180
	CAGCTTCAAG GTGACGATGC CAACTCCCTG CACCTCCTTG CCTCCTGCT GTGAGCACAG	240
	AAGCATTACC ATGACGCTCT GAACATCATC GACATGGCCC TGAGTGAATA CCCAGAAAAT	300
50	TTCATACTAC TGTTTTCCAA AGTGAAGTTG CAGTCACTCT GCCGAGGCCG GGACGARGCA	360
	CTGCTGACTT GTAAGCACAT GCTGCAGATA TGGAAATCCT GCTACAACT CACCAACCCC	420
55	AGTGATTCTG GACGTGGGAG CAGCCTCTTA GATAGAACCA TTGCTGACAG ACGACAGCTT	480
	AATACAATTA CTTTGCCAGA CTTGAGCGAT CCCGAGACAG GCTCCGTCCA TGCCACATCG	540
	GTAGCAGCCT CAAGAGTGA GCAAGGCACTG TCGGAAGTGG CTTCGTCTCT GCAGAGCATG	600
60	CCCCTAAGCA GGGCCCCTG CACCCCTGGA TGACGCTGGC ACAGATCTGG CTCCATGCAG	660

	CTGAAGTCTA TATCGGCATC GGGAAGCCTG CAGAAGCCAC AGCCTGTACC CAAGAAGCTG	720
5	CCAACCTCTT CCCAATGTCC CACAATGTCC TCTACATGCG CGGCCAGATT GCTGAGCTCC	780
	GGGGAAGCAT GGACGAGGCG CGGCGGTGGT ATGAAGAGGC CTTAGCCANT CAGCCCCACC	840
	CACGTGAAGA GCATGCAGCG ACTTGGCCCT GATCCTTCAC CAGYTAGGCC GTACAGTCT	900
10	GGCGGAGAAG ATCCTCCGGG ACGCGGTGCA GGTGAACCTG ACAGCCCACG AGGTCTGGAA	960
	CGGGCTGGGC GAGGTCTCTC AAGCTCAGGG CAACGATGCG GCGGCTACGG AGTGCTTCCT	1020
15	GACAGCCTTG GAGCTGGAGG CCAGCAGCCC CGCGTGCCCC TTCACCATCA TCCCCCGCGT	1080
	GCTCTGAGCA GGCGCCTGCC AGCCTCACCT GCCGCTCAGC CTNCAGAGGC CCTGCCGGGC	1140
	ACCAGGGCTT GTGCCATCGC CCCAAGGGGA TGAATCTGCC GCACTGAGGC CAGGGACGAG	1200
20	TGTTCACTGG GCCACAGTGA ACCAACCAAA CCAACCCCGA ATCATCGCTC TCGCCATGTG	1260
	CGTTTCTCTT GTTTTTTTTG CCAGCCCAAT GGTAGTTTCT GAACCTATTG ACATTGTTCA	1320
25	AAATGGATCA TGTGCCATAT TTTGTTAGTT GACATCTGAG TTTTCAGTAA AATGATTATG	1380
	GAATTAATCA GCAAATGTAG AAGAATATAT TCAAAGTTAA AATTCAGTGG CAGCACAGAT	1440
	TATTTTATC AGAGCTGTAA AGAAAACAAC TGTCCTTTTC TCCCCACCAC CCCTCCTGCC	1500
30	CCACTTTGGC CCAGAAACCA AATGTGAACT TCCTGTCTCC CACCTCAGCA CTAGTCCATG	1560
	CCAGGACACC AGCTGACAAT TTCTTGGTTT TACTGTCAAT AATTGTACCA TGTGATCAAT	1620
35	TACTGTCTC ACTTAGAACA AAGCCTGAGT CCGAGAATAT TTATATTTTA CCAATATATG	1680
	CCTGTTACAA GAGAAGGAAA TATGAGTTAT TTAAGTTTAA CTMTTTTATG TGAATTCAGA	1740
	GTTTATTTAT CGAGGGAAAT ATGTACAAAG AAGCTTCAAA TGGAATATTT ACCGACATTC	1800
40	CTTATACATG ACAGACACTT GGCTACATGG GAAGATGATG TTAATAATAA AATGATTTT	1860
	AAATGGAAAA AAAAAAAAAA AAAAAAN	1886

45

(2) INFORMATION FOR SEQ ID NO: 94:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1774 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

	CTCAGCTACC GTATACAGTA GGACATAACC CCATTTTACA TGCACTACAC TGAGACTTGC	60
60	CTCCTCTCCC CCCACATTGA AGATGTTCTT TTTTCATAAC TATATACTAT TCCATTGCAT	120

	GAATATTCTG TAATTTATTT AATCCCCTAT GGATTGATAA TTAGGTTTCAT TATAGATAGA	180
	AGTGTAATTA ACATTCCTGT ACATGTATTT TGCTACTTGT GTGGGTATTT CTGTAGGATG	240
5	AATAACTAGA AATTTATTGG ATCAGGTTTC ACATTTGCAG TTTTGAAAAC TACTACCAA	300
	AAGATTTTAC CAATTTACAA CTCCATCATT AGTAAGAATG CCTGTTTGCC TATAGTCTGC	360
10	CAACCCTGAA TCCTTAAAAA TTTTGGCCAA TCTGGTAGGC AAAATTTCTT TCTTTTCTTT	420
	GAATATTAAT GAGGAGGAAC ATCTTTTCAT GTTCTTGGC CATTTGCATT TCCTATTATG	480
	AATTGCTTTT GCCCATTTTC CTTTMTTAA TTATGAAAGT CTAATGACTA CCTTCTCATT	540
15	GTATAAAAAA CACAGTTCTT TGAATAGAGA GACCCTTTTC TCCAATGCTA CCAATCACAT	600
	TCCACTTACC ACAGTTTAAAC ATACATCCTC TAGTCACCTT TCCGTACGAA TATACATACA	660
20	CATAAAAACA CTTTMTTACAT AAATAGGATC TCATATTCTG TAGCTTTTAA AAATTTTGGT	720
	CTCAAAAAA GATAACAGGT CTTTAAATTT CTTTAATGGT TGAATATGAT TAAATACTAT	780
	GAAAATGCCA TTATTTATTC CCTTAATTTT TTTCTCTCG CTATTACATT GCCAAAGTAA	840
25	ACATCCTATT CAGATGTCTT TGTGCATGTG TGTGAATATT TCTTTAGTCT GGAGTCCAGT	900
	AAGGTGGATT TTTGGATCAA AGGGTTTGTT CTCTGTCCAC CTTCACTCTT CCCAAAGGCC	960
30	TTCATAACTG TATTTTCACC AAGTGTATGG AGAATGTTCA TTTCCCCATA TAACCATACC	1020
	TACACTTGAT AGTTTTTATC TGTGGGGCGA AAAAGAACCT TTTCTTATTT TGCATTTCCC	1080
	TGATTATAAA AAAAAATGGT GAGATTGGGG TTATTTTCAT GTTTATTTGGC CATTTATAGT	1140
35	TTACTGTGGA TTGTTTGTAT CCCTTACCTG CTTTCTATTG GGTATGTGT GGATATATTG	1200
	TTTTTATTTG TTCAGCATCT CCTTCCCAT CTTCTGGTAA CACAACCTTT ATTTATTTGT	1260
40	GGGGAACCTA TTCCCTGTGG CTTAGGTGAG CATGTGACCA GGCCTGGCCT CCTGAGTCCC	1320
	ACAGCTTCCT AGCCACAGTG ATAAAAGAAT GGGTATATAA CTTAAGCCAG GCTAAGGAAA	1380
	GCCCTTAACA GAACTTCTGC TGAAGTACT GGAAAGAAGG CTTTATGGAG ATCCCAGGAA	1440
45	CCAAGGACCA TGTAAGCCTG AATTTGTGCC ATGTGGAGAG AGTCTGTCTG AGGAGAACT	1500
	CGGATGCTAG CAGAAATGGA AAGAGAACTA AGTTCTGATG TCATTTTCTT GGAGGCCCTA	1560
50	GATCCAGCTG TGCCTAAAGC CTGCCCTACT CCGGACTTTA AAGTTTGTG AGCCAATAAA	1620
	GTCCCTTTCT TGTTTAAGAT AATTGAATTG AGTTTCTGTT CTGATTAATA TAGGTTATTT	1680
	GTATTTTCTT ATTGATTTGT AGAAAACCTT TGTAATTTTA AATTCTAGAC TTTATGCACT	1740
55	ATATAAGTTA ATAAAATTAG CATGGCCTTC CATG	1774

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

10	GGCACGAGCG AAGGCAAGGG GGCACCAGCT CAGGACTGCA TCTGCCTGCC ATTTCCCTTC	60
	CACTCCTCCT TTCTGGAGTC TGACATTAGA AAGCCAGCGA GAAGGAAGAT TCAAACAACC	120
15	AACCTTGATT TCCTGCTTCT CCTTTTCATG AGTGTTCCTG TGGTCTCTGC ACCTCCTTTC	180
	TGTCCCCCGG CAGAGGGCAG TAGAGATGGC CGGCCCAAGG CCTCRGTGGC GCGACCAGCT	240
	GCTGTTTCATG AGCATCATAG TCCTCGTGAT TGTGGTCATC TGCCTGATGT TATACGCTCT	300
20	TCTCTGGGAG GCTGGCAACC TCACTGACCT GCCCAACCTG AGAATCGGCT TCTATAACTT	360
	CTGCCCTGTGG AATGAGGACA CCAGCACCCCT ACAGTGTAC CAGTTCCCTG AGCTGGAAGC	420
25	CCTGGGGGTG CCTCGGGTTC GCCTGGGCCT GGCCAGGCTT GCGGTGTACG GGTCCCTGGT	480
	CCTCACCTTC TTTGCCCCC AGCCTCTCCT CCTAGCCCAG TGCAACAKTG ATGAGAGAGC	540
	GTGGCGSCTG GCAGTGGGCT TCCTGGCTGT KTCCTCTGTG CTGCTGGCAG GCGGCCTGGG	600
30	CCTCTTCCTC TCCTATGTGT GGAATGGGTC ARGCTCTCCC TCCCGGGGCC TGGGTTTCTA	660
	GCTCTGGGCA GCGCCCAGSC CTTACTCATC CTCTTGCTTA TAGCCATGGC TGTGTTCCCT	720
35	CTGAGGGCTG AGAGGGCTGA GAGCAAGCTT GAGAGCTGCT AAAGGCTTAC GTGATTGCAA	780
	GGGTTCAGTT CCAACCATGG TCAGAGGTGG CACATCTGCT CAGCCATCTC ATTTTACAGC	840
	TAACGCTGAT CTCCAGCTCC AGCGATGGAA CCCACTACAG AGGAGGTGGG GCCCCTGTGT	900
40	CAAAGAGGCC GAGGGGCAGC AAGGGCAGMC AGGGCACCTG TGACTTCTTA GTACAAGATT	960
	GTCTGTCTTT CAGGACTTCC AAGGCTCCCA AAGACTCCCT AAACCATGCA GCTCATTGTC	1020
45	ACACCAATTC CTGCTTTAAT TAATGGATCT GAGCAAATCT TCCTCTAGCT TCAGGAGGCT	1080
	GGGAGGGAG TGATTGCTGT CATGGGCCA GACTTCCAGG CTGATTTGCC AAATGCCAAA	1140
	ATGAAACCTA GCAAAGAACT TACGGCAACA AACGAGGACA TTAAAAGAGC GAGCACCTCA	1200
50	GTGTCTCTGG GGACATGTT AAGGAGCTTC CACTCAGCCC ACCATAGTGA GTGGCCCGCC	1260
	ATAAGCCATC ACTGGAATC CAACCCAGG GGTCCAGGAG TGATCTCTGA GTGACTCAAC	1320
55	AAAGACAGGA CACATGGGGT ACAAAGACAA GGCTTGACTG CTTCAAAGCT TCCCTGGACC	1380
	TGAAGCCAGA CAGGGCAGAG GCGTCCGCTG ACAAATCACT CCCATGATGA GACCCCTGGAG	1440
	GACTCCAAAT CCTCGCTGTG AACAGGACTG GACGGTTGCG CACAAACAAA CGCTGCCACC	1500
60	CTCCACTTCC CAACCCAGAA CTTGGAAAGA CATTAGCACA ACTTACGCAT TGGGGAATTG	1560

TGTGTATTTT CTAGCACTTG TGTATTGGAA AACCTGTATG GCAGTGATTT ATTCAATATAT 1620
 5 TCCTGTCCAA AGCCACACTG AAAACAGAGG CAGAGACATG TACTCTGGTG TGATCTCTTG 1680
 TCCTCAGTGT CTCTTCTGGG CTCTGTCCC TCTTGCTTTA TAGCTAGCTG CCCGGGGACC 1740
 AAGGTACAGG TGAAAGCAAG GTAGCAGCTT GCGGGAGGAG GCCTGTCTGG CTTACCAGTC 1800
 10 TATACACTGT GGCCTCAACC TCCAGACAG GGCAGAGAAC TGTGGGCAGC TCGTTTGCTT 1860
 TCTAGGCTGG CTGGAGAGGT GGGAGCTCAT TGATAGACTC ATGATGGAAA CTATTTTGA 1920
 AACAGGCTTC CTCCTTCAGG AGAGATCATG CGGACTAAAC TGTAGCAATT CCAGTGCACC 1980
 15 TGGCAGTGAT CCTTTTCTTT GCAAAGTACT GTCTCTTTGG TTCCAGTAAG TTGGACCACC 2040
 ACATGACATY ATTTTCCCTG GAACCTGGTC ACTGACTAAC ACAGACAATT GGGACTCCAG 2100
 20 AGCCTCAAGA GCCAGGAGAG GGCACAGTAC ATACAGAGGG AGTCAAATGG GATCTCATTT 2160
 TGAGTCCTGC CTTCCGCACA CTCAGAACGG CANCCCCAAG GCCCGGAGTG TCCAGGGCTT 2220
 CTGGCCTGAG GTGAATCTGC CAGGCCCAAG AAGGCACAAA GGTAGGAGCA CAGAGAGCCC 2280
 25 CATTCACACA GCGGKCGGC CCAGCAGCAC CAGTGGAAGC TCAGCTGTCC TCCAGCTGCT 2340
 CTCGGCAGAC AGTTCAGTGC ACAGTTTATG CCCTAGCTGA AAAAGATCTC CCGGACGTAT 2400
 30 TTCAGCACAT CCTCTCCTC CTCCTCCTCA GGGCTCCTGC TACAGGCAGA GCTGGAACCC 2460
 CCCGGCCTCT GGAAGGGCT GAGGCCTGGA GYCACTGCCT GTC 2503

35

(2) INFORMATION FOR SEQ ID NO: 96:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CTGGAAAGCC GAGGGTAGCC GAGCGGGGCG GCGCTCTGG AGCGGCGGGT GTCGGGCTG 60
 CCGTCCGCTC CGCCAGAAGC ACCGAGCAGC CGAGCGGGG CCCGCGCCC TCCTCCTCCA 120
 50 TGAGGCCCGA GTGAGGCGCG GCGGCTATAG CCGACCGCG GCGCTTCCC CCCGCGTCTT 180
 ATCGCGAGCG CACGACMAGC GGGCCCTGGA GGAGGAGGCG GAGGAGGAG AGCATGTCCG 240
 55 ACGGTTTCGA TCGGGCCCCA GGTGCTGGTC GGGGCGGAR CCGGGGCTG GGCCGCGGAG 300
 GGGGCGGCC TRAGGCGGC GGTTTYCCGA AMGARCGGR GCCTGCTGAG CGGRCGCGGC 360
 ACCAGCGCC GCAACCCAAA GCGCGGGCT TYCTGCARCC AMCGCGCTG CGCCARCCA 420
 60

	GGACGACCCC GCCGCCAGGG GCCCAGTGCG AGGTCCCCGC CAGCCCCCAG CGGCCCTTCCC	480
	GGCCCCGGGGC GCTCCCAGAG CAAACGAGGC CCCTGAGAGC TCCACCTAGT TCACAGGATA	540
5	AAATCCCACA GCAGAACTCG GAGTCAGCAA TGGCTAAGCC CCAGGTGGTT GTAGCTCCTG	600
	TATTAATGTC TAAGCTGTCT GTGAATGCCC CTGAATTTTA CCCTTCAGGT TATTCTTCCA	660
10	GTTACACAGA ATCCTATGAG GATGGTTGTG AGGATATATCC TACTCTATCA GAATATGTTT	720
	AGGATTTTTT GAATCATCTT ACAGAGCAGC CTGGCAGTTT TGAAACTGAA ATTGAACAGT	780
	TTGCAGAGAC CCTGAATGGT TGTGTTACAA CAGATGATGC TTTGCAAGAA CTTGTGGAAC	840
15	TCATCTATCA ACAGGCCACA TCTATCCAA ATTTCTCTTA TATGGGAGCT CGCCTGTGTA	900
	ATTACCTGTC CCATCATCTG ACAATTAGCC CACAGAGTGG CAACTTCCGC CAATTGCTAC	960
20	TTCAAAGATG TCGACTGAA TATGAAGTTA AAGATCAAGC TGCAAAAGGG GATGAAGTTA	1020
	CTCGAAAACG ATTTTCATGCA TTTGTACTCT TTCTGGGAGA ACTTTATCTT AACCTGGAGA	1080
	TCAAGGGAAC AAATGGACAG GTTACAAGAG CAGATATTCT TCAGGTGGT CTTGAGAAAT	1140
25	TGCTGAATGC CCTGTTTTCT AATCCTATGG ATGACAATTT AATTTGTGCA GTAAAATTGT	1200
	TAAAGTTGAC AGGATCAGTT TTGGAAGATG CTTGGAAGGA AAAAGGAAAG ATGGATATGG	1260
30	AAGAAATTAT TCAGAGAATT GAAAACGTTG TCCTAGATGC AAAGTGCAGT AGAGATGTAA	1320
	AACAGATGCT CTTGAAGCTT GTAGAAGTCC GGTCAAGTAA CTGGGGCAGA GTCCATGCAA	1380
	CTTCAACATA TAGAGAAGCA ACACCAGAAA ATGATCCTAA CTACTTTATG AATGAACCAA	1440
35	CATTTTATAC ATCTGATGGT GTTCCTTTCA CTGCAGCTGA TCCAGATTAC CAAGAGAAAT	1500
	ACCAAGAATT ACTTGAAAGA GAGGACTTTT TTCCAGATTA TGAAGAAAAT GGAACAGATT	1560
40	TATCCGGGGC TGGTGATCCA TACTTGGATG ATATTGATGA TGAGATGGAC CCAGAGATAG	1620
	AAGAAGCTTA TGAAAAGTTT TGTTTGGAAT CAGAGCGTAA GCGAAAACAG TAAAGTTAAA	1680
	TTTCAGCATA TCAGTTTTAT AAAGCAGTTT AGGTATGGTG ATTTAGCAGA ACACAAGAGA	1740
45	GCAAGAAAAT GTGTCACATC TATACCAAAT TRAGGATGTT GAGTTATGTT ACTAATGTAT	1800
	GCAACTTTAA TTTGTTTTAA CACTATCTGC CAAAATAAAC TTTATTCCTT ATAACTTAAA	1860
50	ATGTGTATAT ATATATAATA GTTTATTATG TACAGTTAAT TCTACTGTTT TGGCTGCAAT	1920
	AAAATCGATT TTGAAATAAA TGAAATGTTG AAAATTTTGC TAGTTGGTTA GATGCTTATC	1980
	CTTTAAATTC TACTTTTTCT GAGGGGAAAA AGTCTTCGTC TGGAAATACA TATTACTGCA	2040
55	AAAATGTAGC ATCCTTTTTT AGGTAGGAGT ATTATAGCTT YCATTTTAGT TKGACATTTA	2100
	GTGTCCCAAT GAATTGAATT TCAATATGA ATCATAATCT TGAAAATCTT TAGCACTAAA	2160
60	GTCTTGGGAA TATATCAACA ACTGATTTAC ATATGCAGAT GCTATTTGNA TACCAAGGGC	2220

TTTTAAATG TCATGGGGG GAAAAACCCA ACTTGGTGGA ACTCCAGCT AAACAACCAA 2280
 GACTTCACTG GAAGATTTAT TCCAATTCTA GGAATTGTC TTTTATTTT TTATTTTTC 2340
 5 AACTGRCTAA CTTCAATTACC TTAAAGCCTA GAACATTATT CTGCTTTATT TATATGGCTT 2400
 TCTCACTTIT ATTTGTAGC AKGGGTGCA TCGACTTTTT TACTAGAGAA TTTTACTAGA 2460
 TATTTGTCAT TCAAGTTTTC ATCTGCTTTA TAATTGATAC ACCTTGAGGG TCACTTTTCT 2520
 10 AATACTTTTA CTATAATGTG GTACCACCTC AGCCCTAATA AATAATATTT TTACCTAATG 2580
 TCAAATCTTT TTCCAGCTAA CTAAAACTG TGTACAAAAG GATTGCTTGT AAATATGCAT 2640
 15 GTAAATAGTT CTGTTAATAA CCCACTGTTT TACATTTGGT ACATCTGTGT CTGCTAATAC 2700
 AGTTAGCTTT CTCACTTTTC TGCTTGTGTG TTCAGTCTGA ATTAAAAATTA GACTTTGAAA 2760
 ATAAAGCTTA AAAAAAAAAA AAAAAAAAAA AAAAAGCTCGA G 2801
 20

25 (2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1631 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

35 ATGGAGCCAA AGACAATCAC TGATGCTTTG GCTTCTAGTA TAATTAAGAG TGTGCTGCCT 60
 AATTTTCTTC CATACAATGT CATGCTCTAC AGTGATGCTC CAGTGAGTGA ACTGTCCCTC 120
 GAGCTGCTTC TGCTTCAGGT TGTCTTGCCA GCATTACTCG AACAGGGACA CACGAGGCAG 180
 40 TGGCTGAAGG GGCTGGTGCG AGCGTGGACT GTGACCGCCG GATACTTGCT GGATCTTCAT 240
 TCTTATTTAT TGGGAGACCA GGAAGAAAAT GAAAACAGTG CAAATCAACA AGTTAACAAT 300
 AATCAGCATG CTCGAAATAA CAACGCTATT CCTGTGGTGG GAGAAGGCCT TCATGCAGCC 360
 45 CACCAAGCCA TACTCCAGCA GGGAGGGCCT GTTGGYTTTC AGCYTTACCG CCGACCTTTA 420
 AATTTTCCAC TCAGGATATT TCTGTTGATT GTCTTCATGT GTATAACATT ACTGATTGCC 480
 50 AGCCTCATCT GCCTTACTTT ACCAGTATTT GCTGGCCGTT GGTAAATGTC GTTTTGGACG 540
 GGGACTGCCA AAATCCATGA GCTCTACACA GCTGCTTGTG GTCTCTATGT TTGCTGGCTA 600
 ACCATAAGGG CTGTGACGGT GATGGTGGCA TGGATGCCTC AGGGACGCAG AGTGATCTTC 660
 55 CAGAAGGTTA AAGAGTGGTC TCTCATGATC ATGAAGACTT TGATAGTTGC GGTGCTGTTG 720
 GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC TGGTCATTGT GGCTCCCTG 780
 60 AGGGTTCCCT TGGATCAGAC TCCTCTTTTT TATCCATGGC AGGACTGGGC ACTTGGAGTC 840

	CTGCATGCCA AAATCATTGC AGCTATAACA TTGATGGGTC CTCAGTGGTG GTTGAAAAC	900
5	GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG ACCTTCACTA TATTGTTTCGT	960
	AAACTGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC TGTGTGTACC TTATGTCATA	1020
	GCTTCTGGTG TTGTTCTTTT ACTAGGTGTT ACTGCGGAAA TGCAAAACTT AGTCCATCGG	1080
10	CGGATTTATC CATTTTTACT GATGGTCGTG GTATTGATGG CAATTTTGTG CTTCCAAGTC	1140
	CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA AGTACCTTGT GGGTCAACGA	1200
15	CTCGTGAAC ACGAACGGAA ATCTGGCAAA CAAGGCTCAT CTCCACCACC TCCACAGTCA	1260
	TCCCAAGAAT AAAGTAGTTG TCTCAACAAC TTGACCTTCC CCTTTACATG TCCTTTTGTG	1320
	TGGACTTCTC TCTTTGGAGA TTTTCCCAG TGATCTCTCA GCGTTGTTTT TAAGTTAAAT	1380
20	GTATTTGACT TGTGTTCTCA GCATTGAGAG AGCAGCGGTG TAAGATTCTG CTGTTCTCCC	1440
	TGGATCTTCT GACATTACTG CTGCTGAGA TTTGTATATG TGTAAATACA AGTTCCTTGA	1500
25	TACCCTAAAA CCTTGGATTA AACAGAATGT GCATTGTACA TCTTTAAACA AAATGTATAT	1560
	TAATTTATTA AATCTAGTTG TCACTTTAAA AAAAAAAAAA AAAAAACTCG AGGGGGGCCC	1620
30	GGTACCCAAA T	1631

(2) INFORMATION FOR SEQ ID NO: 98:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

	CCGAGCTGGG CGAGAAGTAG GGGAGGGCAC GAGCCGCCGC GGTGGCGGTT GCTATCGCTT	60
45	CGCAGAACCT ACTCAGGCAG CCAGCTGAGA AGAGTTGAGG GAAAGTGCTG CTGCTGGGTC	120
	TGCAGACGCG ATGGATAACG TGCAGCCGAA AATAAAACAT CGCCCCCTCT GCTTCAGTGT	180
50	GAAAGGCCAC GTGAAGATGC TGCGGCTGGA TATTATCAAC TCACTGGTAA CAACAGTATT	240
	CATGCTCATC GTATCTGTGT TGGCACTGAT ACCAGAAACC ACAACATTGA CAGTTGGTGG	300
	AGGGGTGTTT GCACTTGTGA CAGCAGTATG CTGTCTTGCC GACGGGGCCC TTATTTACCG	360
55	GAAGCTTCTG TTCAATCCCA GCGGTCTTTA CCAGAAAAAG CCTGTGCATG AAAAAAAGA	420
	AGTTTGTAA TTTTATATTA CTMTTAGTT TGATACTAAG TATTAAACAT ATTTCTGTAT	480
60	TCTTCCAAAA AAAAAAAAAA AAAA	504

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

5	GGCACGAGGG AGGGAGCCCT CTCCGTGCGG TGACTCTTGT GTGCCCTTTA GACAGGCTGG	60
15	CCTGCCGGTT CCACAGGGTA CAGTTAGGAC TTGAGTCTTT CTTTTTCTGT TTTGAGTTGG	120
	TGAGTGAGTG ATAGGGTAAC ATGGGCCTTC AGGATGACCC CTTGGAAC TGCCGAGTTC	180
20	CTTAAATCTC AGCTGGGATC CTGGACCTGG GAGGCCCTG TGAGGGCCAG CTCTGGAAAA	240
	ACCTGGGAGT TGATGCCGGA GCTGTGGAAG AACTCTGCTC GAGGGCAGGG TGCCCTGGAA	300
25	CACTGGTAGT TCTGGGCTG GAGGGAGAG GGGCTCCGGC TTTCTCTGAA ATGAACACTG	360
	CTCTTCAGCA GTTCAAGTAC TTGTCTCAA AACATTTTCT AATTGATTGG TAGGTTTCA	420
	TAAGCATTGT TTCTTTAAGG CATGGAAAGG GAAGAATGCT CAAGCAAGTC ATGTTTGT	480
30	TCAGTGGGAT GGGCCCGCGT TCTCACTGCT GGGGGCTTCC CCTTCATGTG GCACCTTTGT	540
	GCAGGGGCCA CCAGGCAGAC TCTTCCCACC TTCTCCCACT GAAGCACCAA GGGGCTTGGA	600
35	ACCGTAATTT GGCTAATCAG AGGCATTTT TTTGTCTAG TATCTTTCAC ACTTGTCCAA	660
	CCGTCTTATT TTTTAAAAG TTCTGTGCT TGTATTAAAC CGAACTAGA GAGAAATAGT	720
	TTCTGAAGCC AGTTTATTGT GAAGATCCCC AAGGGGAGGT TCGGTAGAGA AAAATAGTAA	780
40	GCTGGTTTAG AAAC TGACGA GGGCAAACAG CCAGGACGCA TTGGAGAGGA ATTTGCCAAA	840
	GATCTACCCT GAGATAACGC CTGTCCAGTG TCTTCACCAC GIGAATAACC AGCGCTCCAA	900
45	AGTGTTTTTC TGCTTTGAAA AAAAAAATTC CACAAGCTTT TAAAGGTGCA TTTAAGAATC	960
	CATGTGACTT TAGAATGAA CTGCCGCCCC TGGCAACTGT CACGTGTGCT AGAAGGTTCT	1020
	ATGCCTCTGG AATGCATGTG ATACTCATCT CCAITTTTGT TCCTTGATTG CATTTTGT	1080
50	CTTTTAGCAG ATCTGTCCCT GTGGGTGGTG TCTAAGAAGT CGGACACCTT GGTTTTGTG	1140
	TTAGATTGAG CTGGGCAGCT GCAATCAGCT TCTTTATATG CAAATTAGGC ACGACCCATC	1200
55	TGTGGTTTCT GGTGGTGGC TAATGAAGTG AGGGGAGGGA GGGATGTCAC CCCAAAAGTA	1260
	GGCCCTCCCA TTGGCTTTGG CCAGGCCAGA CACTTCACAT CGTTTACATG GTTCTGTGTA	1320
	ATTTTAAAGT TTATGTGTAT AAAGCGAAGC TGTTTCTGTG AAACGTATA TTTTGTAAT	1380
60	AAATATATTG CTACTTGAAA AAAAAAAAAA AAAAAA	1416

5 (2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 2847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

15 GGCTAGGACA ATTTTGGTGC TTACCTATC TCTGCAAAGA CTGGAGAATT TGGCATACCA 60
TTAATTACAA CCACCAATCA TATCCAACAA AAGTACCCTA AAAGAAGGAC CAGTGGCCAC 120
TCTCGAAAAA ATTTAAGTAT CAGAAGATTA AAAAGATTTT AGGATTTGGA AGCTTGATTT 180
20 GTCTTTCCCC AATAATCATTT GTTGATCTC CAAATAGTAG CCTTATAITTA GCAATRGACA 240
GATCATTTGGT TCTCCATATC TGATCATATG TTACTACTTT GGAATCAGTA TTTGGGCAAA 300
25 TTCAAGCATT TATGCAGTGG ATATAAATGG AAATATAAAA ATATTTGCCA ACCTGTCTCA 360
GTAACCTATC ATATCTCTGT GNATCCTCAA GGAAAGCACT TTTGCTTTTA CTTAGAAAGC 420
GTTTCAGATT TGCTTTATAG ACTCCTGCTG TCTTCAGTAC CTGATAAAAC TTTAACCAGG 480
30 GAAGCATTAA ACACAGTGCA GCAGCTTTTG CCCAGGCTTC TAAGTTCTCG CCGGCAGCAT 540
TTATCAATGT AAGAACTAGG ATGCTTCCTG CAGTGGCACT ACCTTCCCCT AGAGCTGGAG 600
35 CATGCTGCTT GGCCTTAAGC CCCAGCATGA TGAGGCTTCC CTCCTGCCAG GTCAGTAAAA 660
GTTAGAGAGC TCAGAATTGG GTCTTGCCTG GGTGCAGGTG GCAGGGTTTG CTGAAACCCC 720
TAAAGAGAAG TCACCAAGGG AGGCAGGTAA TGAATGTTTC CAGAATCAGT CKGATACTCA 780
40 TAGCAATTTT TGGCTATCTT TCAAATGTTG AATTTCTGGA TGCTGAGAGG GACTTTGATT 840
TGATATCATTT AAATCCAGGA CAGTCCCAAG AAGTGCTTGG AGTCTCGGCT CTGACAGCCC 900
45 AAGAAGGGAA ATAACCTGTA TTAAGGAACA ACTATGAGCC AGGCCCTGAG CTGTCTCTTA 960
GATAATAAAA CAGATGGGGA GTGGAAGAGT CATTTGCTTC AAGTTATACA GCTAGGAAAT 1020
ACTCAAGCCA AATCTTGAAC GCAGCTCCCC CTAATTCTGT GGACAGGCAC TTTGTACCAC 1080
50 ACACCATGGT CCACCTAAAA ACAGAAGGAT AAAAAGACTT CAGGTTTTC CACTGTGTGC 1140
TGACCATCCC AATTTATGAA TCTTCTTCAA AATGACATTT CACAGTTATA GTTAGGGCTC 1200
55 AGAAATGGCA TTGAGGTAGC CTTATTTCTC CCCTTTAGCA GATGCTTTAA GTACACATTG 1260
CTGACTTGAG CCCACCCCA GGAGTTAGGA GAACATTTCC TTTTTCATGC CATCTTCCAT 1320
AAATAAGGTG TTTCTTGGCC TTCAAAGATA TAGAACTTTG CAGCAGTAGT AAAAGTGAAG 1380
60

	GGTGTCTCTGC TCTCTACTCA ACTTTATTTG AAAATGTCTG CAGCTTCACT CCTGTAGAAA	1440
	AGGAAATCTT CATATTTTAG TAAACTTAGC CGCCAGTGTA CTCTGTGAGG ATGTGGCAAT	1500
5	TCAAAGTCCA GTGAATCTGG CTCTCTTACT GATTCCTGGT TTTAGTGTGT GTGTGGGGG	1560
	AGTGTGTACC TATATATAAA GGACAAGTGT GATATGTGTG TATATGTATA TACATACATA	1620
10	CATGTCCACA CACACACACA CAATATTTGA GAGCTAAGGA AAACCAAAG CAGCCCCCTC	1680
	ATTATCTTGC GTACTACTTC AAAGATTTCT GTCAGCCCTA ATTACAAGTG TCACCATATA	1740
	GTGGGGCTT AGGTACTTGC TTACAGGAAG AGCAATTCCC TAGCAAAGGT CATTAGCTCC	1800
15	TAAGGCACTG AGTCAAAGTG ACAGCCCTGA AGGAAATTGC ACTCCAGCCC TCCTCCAGGA	1860
	TGTCTAATAA GATGGGAAAC TTGGATGCCC AGCCATTTTG GTGACCTGAG AGTCTAACTA	1920
20	CTCCAGTTAG ACCTAAGGGC ACAAATGCAG AATTCATGAC CTGTAGTTG TGGCAGGGTC	1980
	TAGGAAGTCC TCTCTCCCA AGTAGAAAT ATTCTCTTGC CATTCCTGAA ATTCCACATT	2040
	CATATAATGG CTGTGCAATA CATGCTCTC AATAAGAAAA TTAAGTGCAT GTTTACTGTG	2100
25	TGCTGATCAC ATCAGATTTT TATGTTTAA AAAATCTCAT TATGGNTGA GTCCAGCCCA	2160
	GCTCTAAGAG AAAAGAAGG CCCATATGGG AGACTTCAGT CTCATTATTA TTGCCTTTAT	2220
30	CCAGCAGTGC TTATRAAGCC CCCTACCCTG TCCCATTCGA GAAACCATAA GACTCAGGCA	2280
	GTTCCTGATT CTGGAGGCCT GCCTGGTAAG ATAAGATAGT ATAATTGGA ACTGAGAACA	2340
	TACCAGAAAC AGCAGAACGA GGGCCAGAGC AGAAAAATGA AAATAAGTGG AGACACTTAT	2400
35	GGATACATTG GTGCAAAAAA AGCCACGGGS CCCATACTGG GCTTGATATG ACTTTGAGGG	2460
	GACAGCAGAT TAATACTTAA TGAGGGTTAA ACCTGACCAG TCTTTCTACA GTGACAGGCC	2520
40	ACACTGCATG AATGGGGAGA ACCAATGAAT CCATTGTCT CTGCCTATTT TCCTGTGCAC	2580
	AGTCACATTC CCTCCTTAGG AATCTTCCCC TTCCACCTT TACATTAAAC AAGGGAACAC	2640
	TGAATCTTTC AAGGGAATTA CACGTTTGGG TTAATGTTTC AGTATATCAT TTTCATACTG	2700
45	TAAATTATTT TGTAAGAGAG ATTTACTGCT ATCCAGGAT GTTCGGACTT GGTGCCCCTG	2760
	TGCATTTGGA AATCAATAAA CTATTACTGG AAATGCCAAA AAAAAAAAAA AAAAAAAAAA	2820
50	NAAAAAATC GAGGGGGGCC CGTACCC	2847

55 (2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1394 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

5	GAGATTGGTG GAGGAGAGTA AATAATCTAG AGGCAAGAGT TCAGTGAGGG CCAAGGGGGA	60
	CCCCCAGAAA AAGGTATGGA GCTAACTCAT CTCTTTTACA AGGGGTGGCC ATGACTTACT	120
	GTGCAAAGT ACTCAGTGTA TATTTAATGT TGATTGTTGA ATTTTAGTTA CGAGAGGGAA	180
10	GAACAATTTT ACTTCTGTCC TTATTTCACT TGCTGAAAAG CTGTGGGACA AAATGTATGG	240
	AATAGACAAG GCCACTTTCT TTGTGATTTT TGCTTTTCAT GCATATTATT TTATTTACCC	300
15	ATAATTTCCA AGAGGTTTGG CGTTCGCTC TCCTGCTTTT TTCTTTCATC CACCCCTTTT	360
	CTTTTTTTGG AAGGGGGTTA TATATGAGAG TTCATTGAAG AAGTCCAGTG AGGCTGAACT	420
	AAAGGGGCAA GATAGGGCAG TTAATAAAG AGCACTTTAT TTCTTTGAAG CCTTTCTAAG	480
20	AAAGAAATGG GGGTGCAGT GGCTTGAATC TCCCATGATG TTGGAGGGCA CTTAGTGGGG	540
	TIGAAGTATG ACATAATATT TCCCATTTGG GAAAGGAGAA TTTCTCTTAG AGGGTGGCAA	600
25	AATGCCTTTG CCCAGTGTCC CTATTTTAGG CATCTTTTCC TTCCTTATTC CTTCAGTCA	660
	GGGTGTGTCC TATACAAAAC TTCCCATCAG TTCTCTCAA TATTCCCAT TTGTAAATGA	720
	TCACTTCTCT TTTCTAAACC CTTTTCTGT TCAGATCCAT ACAGGATTG CAAGGGTAGG	780
30	ATCATACATG CAAATGCCCC TTGTTTCATCT GTGTCTCTG CAACTAGTC TCATGAAGAA	840
	TTCTGGCGTG CAGCAGGGTA GCTGAAGTTT GGGTCTGGGA CTGGAGATTG GCCATTAGGC	900
35	NTCNCTGAGA TTCCAGCTCC CTTCACCAA GCCCAGTCTT GCTACGTGGC ACAGGGCAAA	960
	CCTGACTCCC TTTGGGCCTC AGTTTCCCCT CCCCTTCATG AAATGAAAAG AATACTACTT	1020
	TTTCTTGTG GTCTAGCATT GCTGGACACA AAGTGTAGTC ATTATTGTG TATTGGGTGA	1080
40	TGTGTGCAAA ACTGCAGAAG CTCACTGCCT ATAAGAGGAA ATAAGAGAGA AAGTGGAGGA	1140
	GAGGGACAAA AGGAGTAATT ATTTGGTATA GATCCACCCA TCCCAACCTT TCTCTCTCA	1200
45	GTCCCTGCTC CTCATGTTTC TGGTTTGGTG AGTCCTTTGT GCCACCACC ATAATGCTTT	1260
	GCATGTCTGC ATCCTGGGAA GGGGTATAT GGTCTCACA GTTGTGTCA TTGTTTTTTT	1320
	GCATGCTTTC TTAATAAAAA AAAAAAAAAA ATGTTTANAG TTTTATCTTA AAAAAAAAAA	1380
50	AAAAAAAAA ACCC	1394

55 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 base pairs

(B) TYPE: nucleic acid

60 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

5 GGMRCGAGGC GGAGTAAAGG GACTTGAGCG AGCCAGTTGC CGGATTATTC TATTTCCCTT 60
 CCCTCTCTCC CGCCCCGTAT CTCTTTTCAC CCTTCTCCCA CCTCGCTCG CGTACCATGG 120
 CGGAGCGTCG GCGGCCACTC AGTCCCATTC CATCTCCTCG TCGTCTTCG GAGCCGAGCC 180
 10 GTCCGCGCCC GCGCGCGCGG GGAGCCCAGG AGCCTGCCCC GCCCTGGGA CGAAGAGCTG 240
 CAGCTCCTCC TGTGCGGTGC ACGATCTGAT TTTCTGGAGA GATGTGAAGA AGACTGGGT 300
 15 TGTCTTTGGA CACGCTGATC ATGCTGCTTT CCTTGGCAGC TTTCAGTGTC ATCARTGTGG 360
 GTTCTTAMC TCATCCTGGC TCTTCTCTCT GTCACCATCA RCTTCAGGAT CTACAAGTCC 420
 GTCATCCAAG CTGTWCAGAA RTCAGAAARA GGCCATCCAW TCCAAAGCCT ACCTGGACGT 480
 20 AGACATTACT CTGTCTCAG AAGCTTTCCA TAATTACATG AATGCTGCCA TGGTGCACAT 540
 CAACAGGGCC CTGAAACTCA TTATTCTCTT CTCTCTGGTA GAAGATCTGG TTGACTCCTT 600
 25 GAAGCTGGCT GTCTTCATGT GGCTGATGAC CTATGTTGGT GCTGTTTTTA ACGGAATCAC 660
 CCTTCTAATT CTGCTGAAC TGCTCATTTT CAGTGTCCTG ATTGTCTATG AGAAGTACAA 720
 GACCCAGATT GATCACTATG TTGGCATCGC CCGAGATCAG ACCAAGTCAA TTGTTGAAAA 780
 30 GATCCCAAGC AAAA 794

35

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

45

TTTGCTTGCT AGTCTGAACC AAAGAGTTGT TTGGGCATTT GCTGTGTTGG CCATTTCTGG 60
 AGCAAGAGGG TCTTCTTCCT CCTTCCCCCA GCCAGCCAGC TGTCTGGGG CCAGGCTTTC 120
 50 CTGGGTGGAA AGAAGTATAC CTTTCCCTGG GGCCCTAGGA TAGCAAAGTG AGCCATAGTG 180
 GGCCAGGCTG CCTTCCATGC TGGGCCCCAG CCCAGGTCTG CACTCGCCTG GATCACCTTC 240
 TTTGAGCCTT AGCCATCTCC TGTGAGGTAG GAATGAACTT GCCAGCCTTC AGGYTCGTTT 300
 55 AGCTATGACC ATCTGTGCGG TCAGGTGACA CTCAGCTCTC CTCCCCAACT CCAGCAGCCT 360
 TTAAGAAGTG TCCCTTTGGC GCCCCCTGGA GGCAGAGCAC TGAGCTGGAC CCTGGGTAGA 420
 60 CTCCACAGG GAGGACGGAG CTGGCCTCAG GAGTGGGACA CCCAGACTTG GCAGGGCCTT 480

CAAGAGGCCT GTGTGGGGC CCCAGGAATC CTTAGCTGAA GCGGGGAGAC TCACTCTCCA 540
 TCTCAGGAAA TTCTAGCCCT TGCCCTCAGG GAGCCACGGT TGAGGGTGAG GCCCAACACC 600
 5 TGCCTTAGGG CCCTGGGTGG GCAAGTCTGG GCCTGGGGT AGGGAGGGAG ACTCAGGCCC 660
 ACACTTGGGT ATTTTCTAAT TTCAGACAAA CACACACTCA GCGCGCACTC ACTGATTCTT 720
 10 ACACATTGCC AAGATTTTAC ACATGTGACC AGGGGCCACC AAAGTCCCTG TGACCTTTGT 780
 GACTAGGATC CTAATTTCTC TATTTTCTCC TGGGTGCTG GGTCTGTGTC ACCTGGGGCA 840
 GTGTGGATAA TGTTTAGTTC TGTGACACTG TTTTTTGGGG GTGGCACCTG GTTCTCCGAT 900
 15 GCCTGGGCTG GTGTCAGGCC CAGGACTGTA GTGCTGGGAG CAGTAAAGCT CAGCTCTGTG 960
 TAATGAGTGA TGCTATGGCT TGCTCGTGTG TTATGATCCA ATCCTTTTCT ACATCAGCCC 1020
 20 TTGTTTGTG TTATGGCTAG TCTTATCTGG CCTGGTTATT TCCTTGCGGG GAGGAGAGGG 1080
 TTTGCTAATC TGCTCCAGC CCAACCTATT ACCACCCAC CTCGCTGGGA CCTACTGCTC 1140
 GGGAGGCAGC AGACAGGGAG CCACCAGCAG TGGCTTCCTG GCCCTGTGCT GGGGTGGGG 1200
 25 GGAAGCTGGG GGCACATGTG GCCCTTGCCT TCTGAGCAGC TCCAGTGCC AGGGCTTTGA 1260
 GACTTTCCCA CATGATAAAA GAAAAGGGAG GTACAGAAGT TCCAATCCC TTTTATTTT 1320
 30 GCTGGTGGT ATCTGTAAAT GTTTAATAAA TATCTGAGCA TGTATCTATC AACGCCAAGA 1380
 ATTTCAAAGT CTCCTTCAAC AATATGAGGC TTTTAGGATG TTTATATTCC TTCATCCCTC 1440
 TTGTTTCCCA GGTTTTGCAG GAAAAAAG TCTGGAATTA TAGATACAGC TTATTATTAA 1500
 35 ATTTGTCTT GCATAAAAAA AAAAAAAAAA AACNCNNGG GGGG 1544

40

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

50

ACCCAGCGT CCGNCTGTC CACCCGGGG CGTGGGASTG AGGTACCAGA TTCAGCCCAT 60
 TTGGCCCCGA CGCCTCTGTT CTCGGAATCC GGGTGTGCG GATGAGGTC CCGGTTCTTA 120
 55 AGGTGGGTG CTGTCCACCC GGGGGCGTGG GAGTGAGGTA CCAGATTGAG CCCATTGGC 180
 CCCGACGCT CTGTTCTCGG AATCCGGGTG CTGCGGATG AGGTCCCGT TCCTAACGA 240
 60 CTGCAAGATG GAGGAAGCG GGAACCTAGG AGGCTGATT AAGATGGTCC ATCTACTGGT 300

CTGTGTCAGGT GCCTGGGGCA TGCAAATGTG GGTGACCTTC GTCTCAGGCT TTCCTGCTTT 360
TCCGAAGCCT TCCCCGACAT ACCTTCGGAC TAGTGCAGAG CAAACTCTTC CCCTTCTACT 420
5 TCCACATCTC CATGGGCTGT GCCTTCATCA ACCTCTGCAT CTTGGCTTCA CAGCATGCTT 480
GGGCTCAGCT CACATTCTGG GAGGCCAGCC AGCTTTACCT GCTGTTCTTG AGCCTTACGC 540
10 TGGCCACTGT CAACGCCCCG TGGCTGGAAC CCCGCACCAC AGCTGCCATG TGGGCCCTGC 600
AAACCGTGGG AGAAGGAGCG AGGCCTGGGT GGGGAGGTAC CAGGCAGCCA ACAGGTTCCT 660
GATCCTTAAC GCCAGNTGCG AGAGAAGGAC CCCAAGTACA GTGCTCTCCG CCAGAAATTC 720
15 TTCCGCTACC ATGGGCTGTC CTCTCTTTC AATCTGGGCT GCGTCTGAG CAATGGGCTC 780
TGTCTCGCTG GCCTTGCCCT GGAAATAAGG AGCCTCTAGC ATGGGCCCTG CATGCTAATA 840
20 AATGCTTCTT CAGAAAAAA AAAAAAAAAA A 871

25 (2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGCAGAGTT ATAGCATGGC ATTCACTTT TTGTTTTATT GCCTCATGAC TTTTTTGAGT 60
35 TTAGAACAAA ACAGTGCAAC CGTAGAGCCT TCTTCCCATG AAATTTTGCA TCTGCTCCAA 120
AACTGCTTTG AGTTACTCAG AACTTCAACC TCCCAATGCA CTGAAGGCAT TCCTTGTCAA 180
40 AGATACCAGA ATGGGTTACA CATTTAACCT GGCAAACATT GAAGAACTCT TAATGTTTTT 240
TTTTTAATAA GAATGACGCC CCACTTTGGG GACTAAAATT GTGCTATTGC CGAGAAGCAG 300
TCTAAAATTT ATTTTTTTAA AAAGAGAAAC TGCCCCATTA TTTTGGTGGG GTTGGTTTTT 360
45 AATTNTAAT NTGAAAAATT TTTTGGGGT TTTTGGGGCC ATGG 404

50

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1542 base pairs

55 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

60

	GTCAGACAGG TGGAGCCGCC GGGGCAGGAG TCTCAAAGAG CCAGGCTCCA GGAGAGGAAG	60
	GGCTCTRCGA GAGGAGAGAG GAGAGCGCTG GAGAGGAGAG GCTGGAGAGT CCTTAGCCAG	120
5	GATGGAGGCT GTTGTGAACT TGTACCAAGA GGTGATGAAG CACGCAGATC CCCGGATCCA	180
	GGGCTACCCT CTGATGGGGT CCCCCTTGCT AATGACCTCC ATTCTCCTGA CCTACGTGTA	240
	CTTCGTTCTC TCACTTGGGC CTCGCATCAT GGCTAATCGG AAGCCCTTCC AGCTCCGTGG	300
10	CTTCATGATT GTCTACAACT TCTCACTGGT GGCACCTCTCC CTCTACATTG TCTATGAGTT	360
	CCTGATGTCG GGCTGGCTGA GCACCTATAC CTGGCGCTGT GACCCTGTGG ACTATTCCAA	420
15	CAGCCCTGAG GCACTTAGGA TGGTTCGGGT GGCCTGGCTC TTCCTCTTCT CCAAGTTCAT	480
	TGAGCTGATG GACACAGTGA TCTTTATTCT CCGAAAGAAA GACGGGCAGG TGACCTTCCT	540
	ACATGTCTTC CATCACTCTG TGCTTCCCTG GAGCTGGTGG TGGGGGGTAA AGATTGCCCC	600
20	GGGAGGAATG GGCTCTTTCC ATGCCATGAT AAACCTCTTC GTGCATGTCA TAATGTACCT	660
	GTACTACGGA TTATCTGCCT TTGGCCCTGT GGCACAACCC TACCTTGGT GGAAAAAGCA	720
25	CATGACAGCC ATTCACTGA TCCAGTTTGT CTTGGTCTCA CTGCACATCT CCCAGTACTA	780
	CTTTATGTCC AGCTGTAACCT ACCAGTACCC AGTCATTATT CACCTCATCT GGATGTATGG	840
	CACCATCTTC TTCACTGTGT TCTCCAACCT CTGGTATCAC TCTTATACCA AGGGCAAGCG	900
30	GCTGCCCGT GCACTTCAGC AAAATGGAGC TCCAGGTATT GCCAAGGTCA AGGCCAACTG	960
	AGAAGCATGG CTTAGATAGG CGCCACCTA AGTGCCCTCAG GACTGCACCT TAGGGCAGTG	1020
35	TCCGTCAGTG CCTCTCCAC CTACACCTGT GACCAAGGCT TATGTGGTCA GGACTGAGCA	1080
	GGGGACTGGC CCTCCCTCC CCACAGCTGC TCTACAGGA CCACGGCTTT GGTTCCTCAC	1140
	CCACTTCCCC CGGGCAGCTC CAGGGATGTG GCCTCAITGC TGTCTGCCAC TCCAGAGCTG	1200
40	GGGGCTAAAA GGGCTGTACA GTTATTTCCC CCTCCCTGCC TTAAAACTTG GGAGAGGAGC	1260
	ACTCAGGGCT GGCCCCACAA AGGGTCTCGT GGCCTTTTTC CTCACACAGA AGAGGTCAGC	1320
45	AATAATGTCA CTGTGGACCC AGTCTCACTC CTCCACCCCA CACTGAAG CAGTAGCTTC	1380
	TGGGCCAAAG GTCAGGGTGG GCGGGGCCT GGAATACAG CCTGTGGAGG CTGCTTACTC	1440
	AACTTGTC TTAATTAAAA GTGACAGAGG AAACCANAAA AAAAAAAAAA AAAAACTCGA	1500
50	GGGGGGCCCG TACCCAAATC GCCGGTATGA TCGTAAACAA TC	1542

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(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2327 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

5	GGTAGCTCAN TGCAGTGAAA TAGTCTTACT GGAAACAAAG CCCTTTATCA AGAATAATTA	60
	ACTCTTCCCT TTTCTTTTGT GAGAGGTGCT TTGTTTCTGA TCGGACCATT TCACTGCAGC	120
10	AAGCAACACA GTATTCTRAG CAGAAGATCG GGAAGTGAGG CCATGTTGCG GAGGGCCAGT	180
	RACATTATCT GGAAGCTGGA GTGTGAGGAA TATGGACTCC ACTCTTCACT ATATTACAR	240
	CGATTGAGAC TTGAGCAACA ATAGCAGTTT TAGCCCTGAT GAGGAAAGGA GAACTAAAGT	300
15	ACAAGATGTT GTACCTCAGG CGTTGTTAGA TCAGTATTTA TCTATGACTG ACCCTTCTCG	360
	TGCACAGACG GTTGACACTG AAATTGCTAA GCACTGTGCA TATAGCCTCC CTGGTGTGGC	420
20	CTTGACACTC GGAAGACAGA ATTGGCACTG CCTGAGAGAG ACGTATGRGA CTYTGCCCTC	480
	AGACATGCAG TGGAAAGTTC GACCGAACTC TAGCATTTCT CATCCACGRG CTTCGAGTTA	540
	TTCTTGGAGA TCAATTGACA GCTGCAGATC TGGTTCCAAT TTTTAATGGA TTTTAAAAG	600
25	ACCTCGATGA AGTCAGGATA GGTGTTCTTA AACACTTGCA TGATTTTCTG AAGCTTCTTC	660
	ATATTGACAA AAGAAGAGAA TATCTTTATC AACCTCAGGA GTTTTGGTG ACAGATAATA	720
30	GTAGAAATTG GCGGTTTCTG GCTGAACTGG CTGAACAGCT GATTTTACTT CTAGAGTTAT	780
	ATAGTCCCAG AGATGTTTAT GACTATTTAC GTCCCATTCG TCTGAATCTG TGTGCAGACA	840
	AAGTTTCTTC TGTTCGTTGG ATTTCTTACA AGTTGGTCAG CGAGATGGTG AAGAAGCTGC	900
35	ACGCGGCAAC ACCACCAACG TTCGGAGTGG ACCTCATCAA TGAGCTTGTG GAGAACTTTG	960
	GCAGATGTCC CAAGTGGTCT GGTCCGCAAG CCTTTGTCTT TGTCTGCCAG ACTGTCAATTG	1020
40	AGGATGACTG CCTTCCCATG GACCACTTTG CTGTGCATCT CATGCCGCAT CTGCTAACCT	1080
	TAGCAAATGA CAGGGTTTCT AACGTGCGAG TGCTGCTTGC AAAGACATTA AGACAACTC	1140
	TACTAGAAAA AGACTATTTT TTGGCCTCTG CCAGCTGCCA CCAGGAGGCT GTGGAGCAGA	1200
45	CCATCATGGC TCTTCAGATG GACCGTGACA GCGATGTCAA GTATTTTGCA AGCATCCACC	1260
	CTGCCAGTAC CAAAATCTCC GAAGATGCCA TGAGCACAGC GTCCTCAACC TACTAGAAGG	1320
50	CTTGAATCTC GGTGTCTTTT CTGCTTCCAT GAGAGCCGAG GTTCAGTGGG CATTCGCCAC	1380
	GCATGTGACC TGGGATAGCT TCGGGGGAG GAGAGACCTT CCTCTCCTGC GGACTTCATT	1440
	GCAGGTGCAA GTTGCCCTACA CCCAATACCA GGGATTTCAA GAGTCAAGAG AAAGTACAGT	1500
55	AAACACTATT ATCTTATCTT GACTTTAAKG KKWAWKMMW KCTCAGMSRA TTATAMITSW	1560
	CWMMRARGSM WYMAAWSCTK SWGCTCYWCC KSRSTGRMKG MMRCTCTAGA AYTRGYRGAK	1620
60	CMYYYKSGCT KMWGGAARKS GGCASGAGCC AGAGACCTGC ATTGCTTTCT CCTGGTTTTA	1680

5 TTTAACAATC GACAAATGAA ATTCTTACAG CCTGAAGGCA GACGTGTGCC CAGATGTGAA 1740
 AGAGACCTTC AGTATCAGCC CTAACCTCTC TCTCCAGGA AGGACTTGCT GGGCTCTGTG 1800
 GCCAGCTGTC CAGCCAGCC CTGTGTGTGA ATCGTTGTG ACGTGTGCAA ATGGGAAAGG 1860
 AGGGGTTTTT ACATCTCCTA AAGGACCTGA TGCCAACACA AGTAGGATTG ACTTAAACTC 1920
 10 TTAAGCGCAG CATATTGCTG TACACATTTA CAGAATGGTT GCTGAGTGTG TGTGTCTGAT 1980
 TTTTTCATGC TGGTCATGAC CTGAAGGAAA TTTATTAGAC GTATAATGTA TGTCTGGTGT 2040
 15 TTTTAACTTG ATCATGATCA GCTCTGAGGT GCAACTTCTT CACATACTGT ACATACCTGT 2100
 GACCACTCTT GGGAGTGCTG CAGTCTTTAA TCATGCTGTT TAAACTGTTG TGGCACAAGT 2160
 TCTCTGTGCC AAATAAAATT TATTAATAAG ATCTATAGAG AGAGATATAT ACACTTTTGA 2220
 20 TTGTTTTCTA GATGTCTACC AATAAATGCA ATTTGTGACC TGTAAAAAAA AAawAAAAAA 2280
 ACTCGAGGGG GGCCCGGTAC CCAAATCGCC GATATGATCT AANCATC 2327

25

(2) INFORMATION FOR SEQ ID NO: 108:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1062 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCCGCCGAG GCGCAACAGC CGTCTGTCA GCTCTGGGTC CAACCGGACT AGCGAANATC 60
 TTCCTCATCC TCATCATCGT CTTCTCATC CGATCTCGG TCCAGGTCCC TCTCCCCCCC 120
 40 ACACAAGAGG TGGCGAAGGT CCAGCTGTAG TTCCTCTGGA CGTCTCGAA GATGCTCTTC 180
 CTCTCTTCG TCATCATCTT CCTCTCGTC TTCCTCATCC TCATCATCCA GTTCTCGAAG 240
 45 CCGCTCAGCA ATCCCCATCC CCCC GCCGA GRAAGTGACA GGAGGCGGCG GTACAGCTCT 300
 TATCGTTCAC ATGACCATTA CCAAAGGCAA AGAGTGCTAC AAAAGGAGCG TGCAATAGAA 360
 GAAAGAAGGG TGGTCTTCAT TGGAAAGATA CCTGGCCGCA TGACTCGATC AGAGCTGAAA 420
 50 CAGAGGTTCT CCGTTTTTGG AGAGATTGAG GAGTGCACCA TCCACTTCCG TGTCCAAGGG 480
 GACAACTACG GCTTCGTCAC TTATCGCTAT GCTGAGGAGG CATTTGCAGC CATTGAGAGT 540
 55 GGCCACAAGC TGCGGCAGGC AGATGAGCAG CCCTTTGATC TCTGCTTTGG GGGCCGAAGG 600
 SWGTNCTGCA AGAGGAGCTA TTCTGATCTT GACTCCAACC GGAAGACTT TGACCCAGCA 660
 CCTGTAAAGA GCAAATTTGA TTCTCTTGAC TTTGACACAT TGTGAAACA GGCCCAAGG 720
 60

AACCTCAGGA GGTAACCTTG GGCCCTTCCC TGCTATCCTT TTTCTCCTTT GGAGGTGCCC 780
 AACCTCCTCC ACCCCCTTCC CCTACTCTAG GGGAGAGAGC TGCTAGTGAG ATGACTGTTT 840
 5 TATAAAGAAA TGGAAAAAAG TGAAATAAAA AATATGTTGA ATCAGATTTT TTAAAAGGGG 900
 TATTTGTTTT TTTATAACAG GTATTGAAAC AAGTTAACTT GCATTCTAT GTAAGATAGG 960
 AGGGGCTGAG GGGATCCCCA GTGTTTGGA CATAAGTCAC TATGCAGACT AATAACATC 1020
 10 AACTAGAGAG NAAAAAAAAA AAAAAAAAAA ATTTAAAAAA CT 1062

15

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 2539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

25

GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGGAAGA 60
 GCACCTACCT GTGTTGGTGA GGTGTTGTTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT 120
 30 AGGCTTCCTG CCTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTC ACACTATGAT 180
 AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCGTGGC CAGGCTTACA TTGWCTCTAG 240
 TGGATTTTCT TCCAAATGA AAGTTGTTGC TTCTAGACTT TYAAGMKMRA TWKCCCMK 300
 35 YWAWCKGAAC AMAMKCTGSW CYTCCWSYGC SKTRRMKRYC GYKSTATRRC WARWKSAYM 360
 CCYKGMTGS RRGTAWYTSK TGCAKAGGG AACAAITGAG GAAGTTTGTT CTTTTTTCCA 420
 40 TCGATCACCA CAACTGCTTT TAGAACTTGA CAACGTAAT TCTGTTCTTT TTCAGAACAG 480
 TAAAGAAAGG GGTAAAGAAC TGAAGGAAAT CTGCCATTCT CAGTGGACAG GCAGGCATGA 540
 TGCTTTTGAA ATTTTAGTGG AACTCCTGCA AGCACTTGT TTATGTTTAT ATGGTATAAA 600
 45 TAGTGACACA AATATTAGAT GGAATAACTA TATAGCTGGC CGAGCATTTG TACTCTGAGT 660
 GCAGTGTCTAG ATTTTGATTT CATGTTACT ATGTTGTTC TTAAAAATGT CCTATCTTTT 720
 50 ACAAGAGCCT TTGGGAAAAA CYYCMAGGGG CAAACCTCTG ATGTCTTCTT TGCKKMSRT 780
 ARMTTTTGAY ATRMARYACT RMTKSAYTY AAYGRWGTGA CWSGAWAATA TTRAASTYTA 840
 TACAATKAAT YWTRRYTSM KRMAGMYAAT CCGAAAYTGT GGMAAMYAAA CTTGATATTC 900
 55 AAATGAAACT CCCTGGGAAA TTCCGCAGAG CTCACCAGG TAACTTGGAA TCTCAGCTAA 960
 CCTCTGAGAG TTAATAATAA GAAACCCTAA GTGTCCCAAC AGTGGAGCAC ATTATTCAGG 1020
 60 AACTTAAAGA TATATTCTCA GAACAGCACC TCAAAGCTCT TAAATGCTTA TCTCTGGTAC 1080

	CCTCAGTCAT GGGACAACCTC AAATTCATA CGTCGGAGGA ACACCATGCT GACATGTATA	1140
5	GAAGTGACTT ACCCAATCCT GACACGCTGT CAGCTGAGCT TCATTGTTGG AGAATCAAAT	1200
	GGAAACACAG GGGGAAAGAT ATAGAGCTTC CGTCCACCAT CTATGAAGCC CTCCACCTGC	1260
	CTGACATCAA GTTTTTTCCT AATGTGTATG CATTGCTGAA GGTCTGTGT ATTCTTCCTG	1320
10	TGATGAAGGT TGAGAATGAG CGGTATGAAA ATGGACGAAA GCGTCTTAAA GCATATTTGA	1380
	GGAACTTTT GACAGACCAA AGGTCAAGTA ACTTGGCTTT GCTTAACATA AATTTTGATA	1440
15	TAAAACACGA CCTGGATTTA ATGGTGGACA CATATATTAA ACTCTATACR AKTAMGTCAG	1500
	MGCTYYCTAC AKAYRAYTCM SWAWMTGTGG AAARYWSSTA MGMSWGCWKK TAMMRRTMCG	1560
	GMWWTYYMK RRTYGAYMYW YGCGWMCAG AAAAAGCCGT AAGGTGTATG TAGACCACTT	1620
20	AATCACTAAA TATCTTTGCC TATAGGACTC CATTGAATAC ATTAGCCATT GATAATCTAC	1680
	CTGTTTAAAT GGGCCCTGTT TGAACCTCA AGCTTTGAAG ACCTACCTGT TCTTCCAGAA	1740
25	GAGAACGTTG AAAGTGCCAT GTTTCCTTTT GCGTGATCTC TGTGTATGGC ACTCTGGAAT	1800
	TGTTTCCAGT TTAATTCATT TTAGACATAG CATTATTAT CACTGTGGAT CTCTACTTGT	1860
	TGGGTGTAT GAATTCCTTG AAGAATATAT TTTGAAGAGG TGTGGGAGGA AGGAATACAT	1920
30	TTTATAAAAT GTTGTAGTGA AGCCCAAT TGACCTTKGA CTAATAGGAG TTTTAAGTAT	1980
	GTAAAAATC TATACTGGAC AGTTACAAGA AATTACCGGA GAAAAGCTTG TGAGCTCACC	2040
35	AAACAAGGAT TTCAGTGTAG ATTTTGTCTT TCTTGAACCT AAAGAAACAA ATGACAAAGT	2100
	TTGAATGGAA AAGCCTGCTG TTGTTCCACA TCTCGTTGCT GTTACATTC CTTGTGGAG	2160
	CCTACATCTT CCTAAGCTTT TTAGCAGGTA TATGTTGAAC ACTTCTGTTT CATGGTTGAG	2220
40	ACAGAATCAG AGGCCATGGA TACTGACAAC TGATTGTCT GTTTTTTTTC TCTGTCTTTT	2280
	TCCATGACTG TTATATACTG CCTCATCTTG ATTTATAAGC AAAACCTGGA AAACCTACAA	2340
45	AATAAGTGT GTGGTTTATC TAGAAAAATA TGAAAAATAT TGCTGTTATT TTTGGTGAAG	2400
	AAAATCAATT TTGTATAGTT TATTTCAATC TAAATAAAAT GTGAATTTTG TTWATTAAA	2460
	AATTWGSAC AAABTBGHGG GGGDTCCAAA CHTWVTCGHG KAAMTCTCT WAARMATYTK	2520
50	ATAAACMSCT TCACAATTC	2539

55 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1751 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

5	AGCATGAAGC CGATGGCCCT GGTGGCCAGT ACCGTCCTGG GCCTGGTGCA AAACATGCGT	60
	GGCTTTGGCG GGATCCTGCT GGTGGTCTAC TACGTATTGG CCATCATTTG GATCAACTTG	120
	TTTAGAGGCG TCATTGTGGC TCTTCCTGGA AACAGCAGCC TGGCCCCCTGC CAATGGCTCG	180
10	GCGCCCTGTG GGAGCTTCGA GCAGCTGGAG TACTGGGCCA ACAACTTCGA TGACTTTGCG	240
	GCTGCCCTGG TCACTCTGTG GAACTTGATG GTGGTGAACA ACTGGCAGGT GTTCTTGAT	300
15	GCATATCGGC GCTACTCAGG CCCGTGGTCC AAGATCTATT TTGTATTGTG GTGGCTGGTG	360
	TCGTCTGTCA TCTGGGTCAA CCTGTTCCTG GCCCTGATTC TGGAGAACTT CCTTCACAAG	420
	TGGGACCCCC GCAGCCACCT GCAGCCCTT GCTGGGACCC CAGAGGCCAC CTACCAGATG	480
20	ACTGTGGAGC TCCTGTTCAG GGATATTCTG GAGGAGCCCG GGGAGGATGA GCTCACAGAG	540
	AGGCTGAGCC AGCACCOCGA CCTGTGGCTG TGCAGGTGAC GTCCGGGCTG CCATCCCAGC	600
25	AGGGGCGGCA GGAGAGAGAG GCTGGCCTAA CACAGGTGCC CATCATGGAA GAGGCGGCCA	660
	TGCTGTGGCC AGCCAGGCAG GAAGAGACCT TTCTCTGAC GGACCACTAA GCTGGGGACA	720
	GGAACCAAGT CCTTTGCGTG TGGCCCAACA ACCATCTACA GAACAGCTGC TGGTGCTTCA	780
30	GGGAGCGGCC GTGCCCTCCG CTTCTTTTA TAGCTGCTTC AGTGAGAAAT CCCTCGTCGA	840
	CTCCACAGGG ACCTTTCAGA CAAAAATGCA AGAAGCAGCG GCCTCCCCTG TCCCCTGCAG	900
35	CTTCGGTGGT GCCTTTGCTG CCGGCAGCCC TTGGGGACCA CAGGCCTGAC CAGGGCCTGC	960
	ACAGGTTAAC CGTGAGTCTG TCTCATCTAT TCACAGCTGG GAATGATACT AATACCTCCG	1020
	ATTTTAGCCC AGCACCACAG GGTACGTTCC AGTTTTCCTC TCTTTCCATA GCTGTAAGGC	1080
40	CCTTTCTGGG AATGGTTCTC ATTCTCCTTA ATCTATTATT GGGTCAGTTT TCCTGCATGT	1140
	CCCCAGCCTC CCATCACTGC CACCCACTCC CCACAGAGAT GCCCTGCTCA TCCGACTGGG	1200
45	GCTTTGACTC CCACACTGTG TACCCCTCTT GTGTGGACGC CCTGCTGCCA AAACCTTCAG	1260
	CAAACAGCTT TCCAAATGGA AGTTGTCACT GTCAGGCCTT TACAATCAGC AACAGCAAAA	1320
	TCTACATGCT GCTGAGGGTC CTGCCCTATT AAGATGCAAT AAATATGTAA GTACATAAAA	1380
50	ACAGCAATAG AAGAAACGTA ATGCTTTATT CTCAAATATG ATGTCTACAT AGAAAAGCCA	1440
	AAATTATTAA GAATAGTAAG AATTCAACCA GCACTTTGGG AGGCCGAGGC GGGTGGATCA	1500
55	TGAGGTCAGG AGATCGAGAC CATCCTGGCT AACAGOGTGA AACCCCGTCT CTAATAAAAA	1560
	TACAAAAAAT TGGCCGGGCG CAGTGGGGG CCCCTGTGGT CCCAGCTACT GGGGAGGCTG	1620
60	AGGCAGGAGA ATGGCGTGAA CCCGGGAAGC GGAGCTTGCA GTGAGCCGAG ATTGCGCCAC	1680

TGCAGTCCGC AGTCCAGCCT GGGCGACAGA GCGAGACTCC GTCTCAAAAA AAAAAAAAAA 1740

AAAAAAAAA A 1751

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(2) INFORMATION FOR SEQ ID NO: 111:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1117 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AATGTTGTGG TGGTAGCATT TGGGTTAATT CTRATTATAG AGTCTCTTGG AGAGCAATGT 60

20

CCATAAACTA ATCCCAAACA ACATTGTCTT TTTRATGTTG TAGTGAACAG CAGAGAATTT 120

CAAAGGACCT TGCTAATATC TGTAAGACGG CAGCTACAGC AGGCATCATT GGCTGGGTGT 180

25

ATGGGGGAAT ACCAGCTTTT ATTCATGCTA AACAACAATA CATTGAGCAG AGCCAGGCAG 240

AAATTTATCA TAACCGGTTT GATGCTGTGC AATCTGCACA TCGTGCTGCC ACACGAGGCT 300

TCATTCGTTA TGGCTGGCGC TGGGGTTGGA GAACTGCAGT GTTGTGACT ATATTCAACA 360

30

CAGTGAACAC TAGTCTGAAT GTATACCGAA ATAAAGATGC CTTAAGCCAT TTTGTAATTG 420

CAGGAGCTGT CACGGGAAGT CTTTTTAGGA TAAACGTAGG CCTGCGTGGC CTGGTGGCTG 480

35

GTGGCATAAT TGGAGCCTTG CTGGGCACTC CTGTAGGAGG CCTGCTGATG GCATTTTACA 540

AGTACTCTGG TGAGACTGTT CAGGAAAGAA AACAGAAGGA TCGAAAGGCA CTCCATGAGC 600

TAAAACTGGA AGAGTGGAAG GGCAGACTAC AAGTTACTGA GCACCTCCCT GAGAAAATTG 660

40

AAAGTAGTTT ACAGGAAGAT GAACCTGAGA ATGATGCTAA GAAAATTGAA GCACTGCTAA 720

ACCTTCCTAG AAACCCCTCA GTAATAGATA AACAAGACAA GGACTGAAAG TGCTCTGAAC 780

45

TTGAAACTCA CTGGAGAGCT GAAGGGAGCT GCCATGTCCG ATGAATGCCA ACAGACAGGC 840

CACTCTTTGG TCAGCCTGCT GACAAATTTA AGTGCTGGTA CCTGTGGTGG CAGTGGCTTG 900

CTCTTGTCCT TTTCTTTTCT TTTTAACTAA GAATGGGGCT GTTGTACTCT CACTTTACTT 960

50

ATCCTTAAAT TTAAATACAT ACTTATGTTT GTATTAATCT ATCAATATAT GCATACATGA 1020

ATATATCCAC CCACCTAGAT TTTAAGCAGT AAATAAAACA TTTCGCAAAA GATTAAAGTT 1080

55

GAATTTTACA GTTAAAAAAA AAAAAAAAAA AAAAAA 1117

(2) INFORMATION FOR SEQ ID NO: 112:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

10 GGCAGAGGTT TTCTTATATT TTAAGTAAAT TTAAAGTGGC TATCAGAATA TTTATTCTTG 60
 TTTGAGACTA CCAACATAAC TACGTGTTGA AGGTGCTTCA CAGAGAATAT ATTGCCCTTTA 120
 ATGTGAAATA ATTTTCACCA ATGTTGCTAA CTTTAATAAA GTATAAAATT TGTAAGATAT 180
 15 TCAGTTAAGT AGTTGGTAAC CCTTTTCTAT TTTAGTAAAA CTTAATGCAT GTTTACTTTT 240
 TTTTGAAAGA TGCAGACAAT CTCTTTGAAC ATGAATTGGG GGCTCTCAAT ATGGCTGCAT 300
 TACTACGAAA AGAAGAAAGA GCAAGTCTTC TTAGTAATCT TGGCCCATGT TGTAAGGCGT 360
 20 TGTGCTTCAG ACGGGATTCT GCAATTCGAA AGCAGCTTGT TAAAAATGAG AAGGGCACCA 420
 TAAACAAGC TTACACGAGT GCTCCAATGG TAGACAATGA ATTACTTCGA TTGAGTCTTC 480
 25 GGTATTTTAA GCGGAAGACT ACTTGCCATG CTCCAGGACA TGAAAAGACT GAAGATAATA 540
 AACTTTCACA GTCCAGTATC CAACAGGAAC TGTGTGTGTC TTAAGACCGA AGTTACAATA 600
 TGGTATTTTT GGTACTGTCT TCCTTCAGCA GTGCATATTC TTTTGCAAAG TTCCTTGGTT 660
 30 TGACAAGCAT TAGTGACAAA GGCAGAAAAG ATTTATCAGC CATGCTAAAA GAGTGAAGAA 720
 TTTTGATCTT TAGAGACACT AGTTTGGGCC AACTTAAGAT TTTACGTAA TTTTACATA 780
 35 GTATTTGACA CTCATGCAAA ATAATGTGAA AACATCTAGA TTTAGTAGTT TATTCTGCGC 840
 CTTTGTGTTAA AACTGAAGAT TTTGGAAAAT GGTGTCACT GCTCTCCAG CCTATGAATA 900
 TTTTGTGAA ATGGAACCAT GGATTTATGT CTGGATCATC CATAAGAAC CAACAATTTT 960
 40 ATTCAAAAAC AATGTGTTCA TCAAAGTAAT TGCTCACATT GTGCAGTACT ATGTTGTACA 1020
 GACCACGTGA AAGGGAATGC TGGTCTAGCT GGCGTGGTAT GTTTATAGGC GAATTCAGC 1080
 45 AGAAGGAAGC CAAAATAGTT TTTTCCTTTT GAAAGTTTTT TAAAAATTAT TTCATGGGTC 1140
 TTTTTTTTAA TTAATATGTG TGCATGTGTA CAATGTATGT TGGGATGTCT TTTGACCCTA 1200
 AATGCTTTTT TTGTTATCAG AGATTGTGTA CTATTTTTAT TTTTAATAAA TGTATCTTCC 1260
 50 CTTTTMAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 1313

55

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
 (B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

5	ACAGGGACAG AATACTTTCT TTCCTTCCTT CAAGTACAAG AAGGCTTTCT CTACCATTTG	60
	CGTCTACACT TTATTTTAAA AGCTATCCTT TTCTAGTAGT ATTTTATCAT GGCAATGGCA	120
10	TGATGACAAC AACAGTCTTT CATTACAGAC TGAAGGAAG CATGTCCTTA CTTAAAATAG	180
	TTCTGCTACT TTCCCTCCTA TTATAAGGAA ATTTTACAGA TTCTAAAAAT ACCTTAATTT	240
15	TTCTTTGATT TTTATTTTAC CAAGTCACAA ATGTCTTTT GAATGTTTGA GAATGTTCT	300
	CATAGAATCA CAAATACTGA CATTTTATTA GATGATTATT TTCCTAGAAT CCCCAAAGAG	360
	CAGTGGCAGT CCATGGCTTG GTTGAAGCTA GAAATTTTCC TGCCCCCTGGT GACCTGGTAA	420
20	GCCTCCTGCT CGGAACCGTG TGAGTGGGTG AGGAAGATGA GAGATGGTCA GATGGAAGAG	480
	AGRAATACAT GAACTGCTCT GGCCTCTCTG GTTCTGTTCT TGGCCCAGAG TTTTGTAAAA	540
	GCAGCGGANA TNGACTGACT TCACATGCTC AGCTTTCTCA GCCTTTTGTT TATTTTGTG	600
25	TCCTTAGATT TCCCTGTTGT AAAAGGGGCA AGAAAAGTAA CTCATCATCT CTAACACACC	660
	ATGGCAGCTT AGCCAGGTAG TCTTAGTGGT GGTGTTTAGG CATAAGATAT GCTGATCATC	720
30	AGTCTCAGGC CACAGTTTCC TTACTAATC GTCCAGCTTG AGTGTCTGT TCTCTTCTG	780
	CCCATTTTCTT TGAACCTCCT GCTCTAGCCT TGGCGGAGGG AGAGTGCTAT TTGCTTTTGT	840
35	TCTCCCTCTG TCTTAGGAAA AGCCATCTTT AATATAGTTC TTCACCACTG TTGGGGTTGT	900
	TTTGIGATT TTTTCTCTT CCGAAGAACT CCTGGTTGTT ATTGGAATTT GTATTTTAAT	960
	ACAAATTATT GAATTTTATA AGCTTGTA CAATATTTAA TTAGTGTGAA AGGAAACAAA	1020
40	GAATGCAGGA AAAATAATTT AATATCAACC TCAGTTGACA AGGTGCTCAG ATTATTCAAT	1080
	TCGGGATCCT CCTTTTGTTA GGTTTTGAG ACAACCCTAG ACCTAACTG TGTACAGAC	1140
45	TTCTGAATGT TTAGGCAGTG CTAGTAATTT CCTCGTAATG ATCTGTATAT TACTTTCCTA	1200
	TTCTTTATTC CTCTTCTTC TGAAGATTAA TGAAGTTGAA AATTGAGGTG GATAAATACA	1260
	AAAAGGTAGT GTGATAGTAT AAGTATCTAA GTGCAGATGA AAGTGTGTTA TATACATCCA	1320
50	TTCAAAATTA TGCAAGTTAG TAATTACTCA GGGTTAACTA AATTACTTTA ATATGCTGTT	1380
	GAAYCTACTC TGTTCTTGG CTAGAAAAAA TTATAAACAG GACTTTGTAG TTTGGGAAGC	1440
55	CAAAATGATA ATATTCTATG TTCTAAAAGT TGGGCTATAC ATAAATTATT AAGAAATATG	1500
	GATTTTATTT CCCAGGATAT GGTGTTTCAAT TTATGATATT ACGCAGGATG ATGTATTGAG	1560
	TAAAATCAGT TTTGTAAATA TGTAAATATG TCATAAATAA ACAATGCTTT GACTTATTTT	1620
60	CAAAAAAATA AAAAAATAAA NTTCGAGGGG GGGC	1654

5 (2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

15 GGCAAACTTT CCCCAANGC TTCGAAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT 60
GGGTTGCGNC GCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT 120
CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC 180
20 CTGGMCTCA TCTTCTGCG CCGACCTGCG CGGGTAAGG GGWAGTTTCA GACTGTGAAG 240
GACGTCGTGC TGGACTGCCT GTTGGACTTC TTACCCGAGG GGTGAACAA AGAGAAGATC 300
25 ACACCACTCA CGCTCAAGGA AGCTTATGTG CAGAAAATGG TTAAAGTGTG CAATGACTCT 360
GACCGATGGA GTCTTATATC CCTGTCAAAC AACAGTGGCA AAAATGTGGA ACTGAAATTT 420
GTGGATTCCT TCCGGAGGCA GTTTGAATTC AGTGTAGATT CTTTTCAAAT CAAATTAGAC 480
30 TCTCTCTGCG TCTTTTATGA ATGTTTCAGAG AACCCAATGA CTGAGACATT TCACCCACA 540
ATAATCGGGG AGAGCGTCTA TGGCGATTTT CAGGAAGCCT TTGATCACCT TTGTAACAAG 600
35 ATCATTGCCA CCAGGAACCC AGAGGAAATC CGAGGGGAG GCCTGCTTAA GTACTGCAAC 660
CTCTTGGTGA GGGGCTTTAG GCGCCCTCTT GATGAAATCA AGACCCTTCA AAGGTATATG 720
TGTTCCAGGT TTTTCATCGA CTTCTCAGAC ATTGGAGAGC AGCAGAGAAA ACTGGAGTCC 780
40 TATTTGCAGA ACCACTTTGT GGGAAATGGA AGACCGCAAG TATGAGTATC TCATGACCCT 840
TCATGGAGTG GTAAATGAGA GCACAGTGTG CCTGATGGGA CATGAAAGAA GACAGACTTT 900
45 AAACCTTATC ACCATGCTGG CTATCCGGT GTTAGCTGAC CAAAATGTCA TTCCTAATGT 960
GGCTAATGTC ACTTGCTATT ACCAGCCAGC CCCCTATGTA GCAGATGCCA ACTTTAGCAA 1020
TTACTACATT GCACAGGTTT AGCCAGTATT CACGTGCCAG CAACAGACCT ACTCCACTTG 1080
50 GCTACCTGTC AATTAAGAAT CATTTAAAAA TGTCCTGTGG GGAAGCCATT TCAGACAAGA 1140
CAGGAGAGAA AAAAAAAAAA AAAAAAAAAA A 1171

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(2) INFORMATION FOR SEQ ID NO: 115:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

	GGTCTGCGCC GGAAGTGCAT GAGCTGCCGA TGTGGTGCTT AGTGATTGCG GTTTCGGTCCG	60
10	CTCTCCCGTG TTTCCCGGGC TGGGTATTTG CCTCGCACCA TGGCGCCCAA GGGCAAAGTG	120
	GGCACGAGAG GGAAGAAGCA GATATTGAA GAGAACAGAG AGACTCTGAA GTTCTACCTG	180
15	CGGATCATAC TGGGGGCCAA TGCCATTAC TGCCTGTGA CGTTGGTCTT CTMTTACTCA	240
	TCTGCCCTCAT TTTGGGCTG GTTGGCCCTG GGCTTTAGTC TGGCAGTGTA TGGGGCCAGC	300
	TACCACTCTA TGAGCTCGAT GGCACGAGCA GCGTTCTCTG AGGATGGGGC CCTGATGGAT	360
20	GGTGGCATGG ACCTCAACAT GGAGCAGGGC ATGGCAGAGC ACCTTAAGGA TGTGATCCTA	420
	CTGACAGCCA TCGTGCAGGT GCTCAGCTGC TTCTCTCTCT ATGTCTGGTC CTCTGGCTT	480
25	CTGGCTCCAG GCGGGGCCCT TTACCTCCTG TGGGTGAATG TGCTGGGCC CTGGTTCACT	540
	GCAGACAGTG GCACCCAGC ACCAGAGCAC AATGAGAAAC GGCAGCGCCG ACAGGAGCGG	600
	CGGCAGATGA AGCGTTTATA GCCATTGACA TTGTGGCCAC AGGCCACTGG CCCTGGGTGG	660
30	CTCTGTCAAG GTGCACAGCC CTCATGCCT GGAGCAATGA GGGTCTAGTC CAGGGGCCAA	720
	AAGCAGTCTG AGGTATTGGG TATACTTATA CTCTATAGGG TCGTTGAATA AATGGCTTAG	780
35	AATGTGAAAA AAAAAAAAAA AAAAACTCG AGGGGGGCC GGTACCCAAT TTCNCCTANA	840
	AT	842

40

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 1640 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

50

	GGCACGAGGC GCGGCAGCG GTGGCGGCGG CGCCCCCGG CGGGAGCCGT TCCCTTTCCC	60
	GTGCGGGAGC GCGGGGYCGG GGCCAGGGG ACCCGGGCC ACGGAGAGCG GGAAGAGGAT	120
55	GGATTGCCCG GCCCTCCCC CCGATGGAA GAAGGAGGAA GTGATCGAA AATCTGGCT	180
	AAGTCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAGAAGT TCAGAAGCAA	240
60	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGATCTC AGCAGTTTTC ACTTCAGAAC	300

	TGGAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT	360
	CAATCAAAAT AAGGGTAAAC CAGACTTGAA ATACAACATT GCCAATTAGA CAAACAGCAT	420
5	CAATTTTCAA ACAACCGTA ACCCAAAGTC ACAAATCATC CTAGTAATAA AGTGAAATCA	480
	GACCCACAAC GAATGAATGA ACAGCCACGT CAGCTTTTCT GGGAGAAGAG GCTACAAGGA	540
10	CTTTAGTGCA TCAGATGTAA CAGAACAAAT TATAAAAACC ATGGAAC TAC CCAAAGGTCT	600
	TCAAGGAGTT GGTCCAGTAG CAATGATGAG ACCCTTTTAT CTGCTGTTGC CAGTGCTTTG	660
	CACACAAGCT CTGCGCCAAT CACAGGGCAA GTCTCCGCTG CTGTGGAAAA GAACCTGCTG	720
15	TTTGGCTTAA CACATCTCAA CCCCTCTGCA AAGCTTTTAT TGTACAGAT GAAGACTCAG	780
	GAAACAGAAG AGCGAGTACA GCAAGTACGC AAGAAATTGG AAGAAGCACT GATGGCAGAC	840
20	ATCTTGTCGC GAGCTGCTGA TACAGAAGAG ATGGATATTG AAATGGACAG TGGAGATGAA	900
	GCCTAAGAAT ATGATCAGGT AACTTTTCGAC CGACTTTCCC CAAGAGAAAA TTCCTAGGAA	960
	ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA	1020
25	TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTATAGTG TATTTTIGAT GTATATATCT	1080
	ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAAATA	1140
30	TCAAGCAGGA CCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG	1200
	TAGCACTTAC GTAAAACATT TGTTTCCCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC	1260
	TAAATAAATT TOCCAGTTAA AGATTATGT GACTTCACTG TATATAAACA TATTTTATA	1320
35	CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCGTCA CTGTAAAGAC AAATAAATGA	1380
	TTATATTCCA CAGAAAAAAA AAAAAAAAAAW MWSTYGARRR GSRGCMCRSW AYMMARWCC	1440
40	CCWMRTWRGS MKTCSTMTKA YTTACATTCA ACTCTGATCC CGGGGCCTTA GGTTTGACAT	1500
	GGGAGGTGGG AGGAAGATAG CGCATATATT TGCAGTATGA ACTATTGCCT CTGGGACGTT	1560
	GTGAGGAATT GTGCTTTCAC CAGAAATTCT AAGGATTTCT GGCTTAAATA TCACCTAGCC	1620
45	TGTGGTAATT TTTTTCCT	1640

50 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 952 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

60 TGAATTTAGN AAACACTTTG GAAACTCAT AACCTCATCA GAAACTGCCT TTAGCCACAC 60

TCCTGACCTT CTAGATGAGT AACAAAAAAA TGAAATAAGT TCTTGGAAT TAAGCCATTT 120
 ATTTTAATTT GCTATTTTTT TCAATGTTCT AGGTATCTTT AAATTTGTTA TTGTGGAATC 180
 5 ATTTTCTGC CAGATACCTT TATCAAAATT ATTGGCCTCA TGAGAGCTGA AGTAAGTCAG 240
 CTTTTTGGTG AACTTTAGTG GACTTCTGTG AGATTGTAGT TGTACTTTGT ATCTCTAAAT 300
 10 CTAAAGATAG TTTTTTAAAA CTCCCAAAGA AAATCTGCTC TCCTTTCTGA TCTAAAACT 360
 CATCTTTGGG GTAAAGAGTT AAGTGTCCAA AGGTTGTCAC AGTTCATGAG GTCAGAGGGA 420
 GCTAGCCTGG CACCTGGACT CTGCCCATCC ACAGCTGACA GATTCCAACA GAAGTGATT 480
 15 TAAATTCCTC AGTAGACAAT GCTGGGTAAG GGAGGGGTA GGGCTGGGTT ATTAAGATAC 540
 AGGCTGCTGT ATTTTACATT GGTGTGGGG GAAGGGGAGC CTGGAGAAAA CAAAGTCACT 600
 20 ATTCCTTTT TTGAACAGG AAAAAAATT ATTTTGTGTT CAGTAAAAAT GGTAGAGAAT 660
 TCCAATGTCC CTAGCCACAA GGGACCAGTT CCACTGAGAA GTGAACAGTG GGAATCAAA 720
 ATTTTCAGAA CATTGGGGGA AGGGAAAATT GGCTTTCTCT TAATTGGCAG ATGTTCCAGT 780
 25 GGGGSGGGG GGCTCTGTTT TTGTTGGGAT GTGTTATGTT GTATGTACGC ATATATGGAC 840
 CGGAGTCTGC TGAGTTTATA AGGTTCCAAA AATATGGTAA AATCTTGGTT TTTGTTAATT 900
 30 TATCTCAATA AAAGCCCACT GGRACCTCAA AAAAAAAGA AAAAAAGA NN 952

35 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

45 GACGTCATAG GTAAACAGGC TCTGTATCCG TGGCAGCGC CGTGGCAGGC TGGCTGGGTA 60
 CCGGCTGTCG CTGACCCAGG AGAAGCTGCC TGTCTACATC AGCCTGGGCT GCAGCGCGCT 120
 GCCGCCGCGG GCCCGGCAGC TGAACATATG TCTCTTCAGG GCGGCACCG TGTTGCATT 180
 50 ATCTTTGTAC CCCCAGCATC TAGCAGTGTG GGCATGTAGT AGGCACTCAA GAAATGTGTG 240
 TTGAATGAAC GATGCCTGTG ACAAGCAAGC GGACTTTATT CTTTCCTGAC CCTTGCTCCT 300
 55 ATGACACACC TCCTCCTGAC TGCCACTGTC ACTCCTTCAG AGCAGAACTC CTCTAGGGAA 360
 CCTGGATGGG AAACAGCCAT GGCCAAGGAC ATCCTGGGTG AAGCAGGGCT AACTTTGAT 420
 GAACTGAACA AGCTGAGGGT GTTGACCCA GAGGTTACCC AGCAGACCAT AGAGCTGAAG 480
 60

	GAAGAGTGCA AAGACTTTGT GGACAAAATT GGCCAGTTTC AGAAAATAGT TGGTGGTTTA	540
	ATTGAGCTTG TTGATCAACT TGCAAAAGAA GCAGAAAATG AAAAGATGAA GGCCATCGGT	600
5	GCTCGGAACT TGCTCAAATC TATAGCAAAG CAGAGAGAAG CTCAACAGCA GCAACTTCAA	660
	GCCCTAATAG CAGAAAAGAA AATGCAGCTA GAAAGGTATC GGGTTGAATA TGAAGCTTTG	720
	TGTAAAGTAG AAGCAGAACA AAATGAATTT ATTGACCAAT TTATTTTTC A GAAATGAACT	780
10	GAAAATTTTCG CTTTTATAGT AGGAAGGCAA AACAAAAAAA AGCCTCTCAA AACCAAAAAA	840
	ACCTCTGTAG CATTCAGCG GCTTGACCAA TGACCTATGT CACAAGAGGT GCGGTGTAAG	900
15	GAATGCAGCC CCCTGAAGAC AGCACTACAA GTCTGGGGGA GCCAGTTTTA ACATCAGTGC	960
	ACAGCTGCTG CTGGTGGCCC TGCAGTGAC GTTCTCACCT CTTATGCTTA GTTGGA ACTA	1020
	AGCAGTTTGT AAACCTTCAT CCTTTTPTT GTAAATTCAC AAAGCTTTGG AAGGAGAAGC	1080
20	AATAAATTTT TGTTTTCAAA TGGCTTGATG TACCTTTTTT CCTGTTGCTC TTGAAATATG	1140
	TTTAACTCCT CATGAGAGAA CCCTGGATTC TCTATCCCT AGTCCACAAA ACAACCAGG	1200
25	CAGTGGTCAG CAGCTACCTT TNATTTGGAT CACACACGTG AGTCAGACAG TACCAC	1256

30 (2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

40	GGCCGTAGCA GCCGGGCTGG TCCTGCTGCG AGCCGGCGGC CCGGAGTGGG GCGGCGGCAT	60
	GTACCTTCCA CATTGAGTAT TCAGAAAGAA GTGATCTGAA CTCTGACCAT TCTTTATGGA	120
	TACATTAAGT CAAATATAAG AGTCTGACTA CTTGACACAC TGGCTCGAGC AAACATGAAC	180
45	GTTGGAGTTG CCCACAGTGA AGTGAATCCA AATACCCGTG TCATGAACAG CCGGGGTATG	240
	TGGCTGACAT ATGCATTGGG AGTTGGCTTG CTTCATATTG TCTTACTCAG CATTCCCTTC	300
50	TTCAGTGTTT CTGTTGCTTG GACTTTAACA AATATTATAC ATAATCTGGG GATGTACGTA	360
	TTTTTGATG CAGTGAAAGG AACACCTTTC GAAACTCCTG ACCAGGGTAA AGCAAGGCTC	420
	CTAACTCATT GGAACAACCT GGACTATGGA GTACAGTTTA CATCTTCACG GAAGTTTTTC	480
55	ACAATTTCTC CAATAATTCT ATATTTTCTG GCAAGTTTCT ATACGAAGTA TGATCCAACT	540
	CACCTCATCC TAAACACAGC TTCTCTCCTG AGTGTACTAA TTCCCAAAAT GCCACA ACTA	600
60	CATGGTGTTT GGATCTTTGG AATTAATAAG TATTGAAATG TTTTGAACT GAAAAAAAT	660

5 TTTACAGCTA CTGAATTTCT TATAAGGAAG GAGTGGTTAG TAAACTGCAC TGTTTCTSTG 720
 ATAATGTGAA ATGAGAAGTA TTTACATTGG AGGGCCAATG GCTGGTCCTT CAAGTGCTGT 780
 TTTGAAGTGC AGATTTCCAT TAAATGATGC CTCTGTTTAA TACACCTGGT ACATTTCTGA 840
 AGAGGGGCTT TATAAGCAGG CTGGGCAGGC CCAGCTTATA AGTTAAAGGG CATCACAGTG 900
 10 AGGGTGTAGT AGATAAATTC AAGGAAATAA GAGATTGTGA AGAACTAGG ACCAGCTTAA 960
 CTTATAATGA ATGGGCATTG TGTTAAGAAA AGAACATTTT CAGTCATTCA GCTGTGGTTA 1020
 TTTAAAGCAG ACTTACATGT AAACCGAAT CCTCTCTATA CAAGTTTATT AAAGATTATT 1080
 15 TTTATTACCG TAAAAAANA AAAAAAANA AAAAAAANA AAAAAAANA AAAAAAANA 1140
 GAN 1143

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(2) INFORMATION FOR SEQ ID NO: 120:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CAGGCCCCGG CCCCCACCC ACGTCTGCGT TGCTGCCCCG CCTGGGCCRG GCCCAAAGG 60
 35 CAAGGACAAA GCAGCTGTCA GGGAACCTCC GCCGGAGTCG AATTTACGTG CAGCTGCCGG 120
 CAACCACAGG TTCCAAGATG GTTTGCGGGG GCTTCGCGTG TTCCAAGAAC TGCCGTGTGG 180
 CCCTCAACCT GCTTTACACC TTGGTTAGTC TGCTGCTAAT TGGAATTGCT GCGTGGGGCA 240
 40 TTGGCTTCGG GCTGATTTCC AGTCTCCGAG TGGTCGGCGT GGTCAATGCA GTGGGCATCT 300
 TCTGTTCCT GATTGCTTTA GTGGGTCTGA TTGGAGCTGT AAAACATCAT CAGGTGTTGC 360
 45 TATTTTMTTA TATGATTATT CTGTTACTTG TATTTATTGT TCAGTTTCT GTATCTTGG 420
 CTTGTTTACC CCTGAACCAG GAGCAACAGG GTCAGCTTCT GGAGGTTGGT TGGAACAATA 480
 CGGCAAGTGC TCGAAATGAC ATCCAGAGAA ATCTAACTG CTGTGGGTTC CGAAGTGTTA 540
 50 ACCCAAATGA CACCTGTCTG GCTAGCTGTG TFAAAAGTGA CCACTCGTGC TCGCCATGTG 600
 CTCCAATCAT AGGAGAATAT GCTGGAGAGG TTTTGAGATT TGTGGTGCC ATTGGCCTGT 660
 55 TCTTCAGTTT TACAGAGATC CTGGGTGTTT GGCTGACCTA CAGATACAGG AACCAGAAAG 720
 ACCCCCGCGC RAATCCTAGT GCATTCCCTT GATGAGAAAA CAAGGAAGAT TTCCTTTCGT 780
 ATTATGATCT TGTCACTTT CTGTAATTTT CTGTTAAGCT CCATTTGCCA GTTTAAGGAA 840
 60

	GGAAACACTA TCTGGAAAAG TACCTTATTG ATAGTGGAAT TATATATTTT TACTCTATGT	900
	TTCTCTACAT GTTTTTTCTT TTCCGTTGCT GAAAAATATT TGAACTTGT GGTCTCTGAA	960
5	GCTCGGTGGC ACCTGGGAAT TFACTGTATT CATTGTGGG CACTGTCCAC TGTGGCCTTT	1020
	CTTAGCATTT TTACCTGCAG AAAAAGTTTG TATGGTACCA CTGTGTTGGT TATATGGTGA	1080
10	ATCTGAACGT ACATCTCACT GGTATAATTA TATGTAGCAC TGTGCTGTGT AGATAGTTCC	1140
	TACTGGAAAA AGAGTGGRAA TTTATTAAAA TCAGAAAGTA TGAGATCCTG TTATGTTAAG	1200
	GGAAATCCAA ATTCCCAATT TTTTTGGTC TTTTAGGAA AGATGTGTTG TGGTAAAAAG	1260
15	TGTTAGTATA AAAATGATAA TTWACTKGTA GTCTTTTATG ATWACACCAA TGTATTCTAG	1320
	AAATAGTTAT GYCYTAGGAA ATTGTGGTTT AATTTTGGAC TTTTACAGGT AAGTGCAAAG	1380
20	GAGAAGTGGT TTCATGAAAT GTTCTAATGT ATAATAACAT TTACCTTCAG CCTCCATCAG	1440
	AATGGAACGA GTTTTGAGTA ATCAGGAAGT ATATCTATAT GATCTTGATA TTGTTTATA	1500
	ATAATTTGAA GTCTAAAAGA CTGCATTTT AAACAAGTTA GTATTAAATGC GTTGGCCAC	1560
25	GTAGCAAAA GATATTTGAT TATCTTAAAA ATTGTTAAAT ACCGTTTCA TGAAAGTTCT	1620
	CAGTATTGTA ACAGCAACTT GTYAAACCTA AGCATATTTG AATATGATCT CCCATAATTT	1680
30	GAAATTGAAA TCGTATTGTG TGGCTCTGTA TATTCTGTTA AAAAATTAAA GGACAGAAAC	1740
	CTTCTTTTGT GTATGCATGT TTGAATTAAA AGAAAGTAAT GG	1782

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(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

45

	GTGGCTGCA GATTGTGGT GCGTCTGAG CCGTCTGTCC TGCGCCAAGA TGCTTCAAAG	60
	TATTATTAAA AACATATGGA TCCCATGAA GCCCTACTAC ACCAAAGTTT ACCAGGAGAT	120
50	TTGGATAGGA ATGGGGCTGA TGGGCTTCAT CGTTTATAAA ATCCGGGCTG CTGATAAAAG	180
	AAGTAAGGCT TTGAAAGCTT CAGCGCCTGC TCCTGGTCAT CACAACCAGA TTTACTTGGA	240
55	GTACATGTGA AAGAAAACGT CAGTCTGCCT GTAAATTTCA GCAAGCCGTG TTAGATGGGG	300
	AGCGTGAAC GTCACGTGAC ACTTGATATA GTACCGTTTA CTTCATGGCA TGAATAAATG	360
	GATCTGTGAG ATGCACTGCT ACCTGGTACT GCTTTCAGTG TGTCCCCCT CAGCCCTCCG	420
60	GCGTGTGAGG CATACTCTGA GTAGATAATT TGTCATGCAG CGCATGCAAT CAGAATCTCA	480

CTGAGCCACC CATCATTTGTG AAATAATTAC CTCAGTTGTA CAGGACTTGG TGATCAGGAT 540
 CCAGGCACTC ACTTGTATTC TACTGCTCAA TAAACGTTTA TTAAACTTGA AAAAAAAAAA 600
 5 AAAAAAAAAA 610

10

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

20

GGTACGCCTG CAGGTACCGG TCCGGAATTC CGGGTCGCCC ACGCGTCNGG CCACGCGTCC 60
 ACCACGCGT CCGSCCAGC GTCGAGCCG AGCCGACTG GTCAGGATGA TCACGACGT 120
 25 GCAGCTCGCC ATCTTCGCCA ACATGCTGGG CGTGTGCTC TTCTTGCTG TCGTTCTCTA 180
 TCACTACGTG GCCGTCAACA ATCCAAGAA GCAGGAATGA AAGTGGCGCT TTCTCCGCC 240
 CAGGGTTCCA GGACATAGTC TGAGGCAAGA TGGAGGGTAT GAGGGGCCCT CACACTTCAC 300
 30 TTCATCCCTT CTACCCATCA CAACATACAA AGCAACTACA CCTGGATTTT TCCAAACAAC 360
 TTTTATTTCC TCAGAGTCCT CCTTAATCCT ATGGAACAAG AAGCTGCCAC TGAATAGGGC 420
 35 CCAGTATAGG GGCTTGCTTT TCTACTCCCT CCCCCAATA TAAAAATATA GACTTTTAA 480
 AAAAAAAAAA AAAAANTTCG NGGGGGGSCC GGTACCCATC CCCCTA 526

40

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 2081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

TGTACCGGTC CGGAAATTCC CGGGTCGACC CACGTCGTC GGGGAACATG GCGGCTKCGG 60
 AGCCGGCGGT CCTTGCCTC CCCAACAGCG GCGCCGGGGG CGCGGGGGCG CCGTCGGGCA 120
 55 CAGTCCCGGT GCTCTTCTGT TTCTCAGTCT TCGCGGACC CTCGTGGTG CCACACGGG 180
 CGGGCTACGA GCTGCTCATC CAGAAGTTCC TCAGCCTGTA CGGCGACCAG ATCGACATGC 240
 60 ACCGCAAATT CGTGGTGCAG CTGTTGCGCG AGGAGTGGGG CCAGTACGTG GACTTGCCCA 300

	AGGGCTTCGC GGTRAGCGAG CGCTGCAAGG TGCCTCTCGT GCCGYTGCAG ATCCAGCTCA	360
5	CTACCCTGGG AAATCTTACA CCTTCAAGCA CTGTGTTTTT CTGCTGTGAT ATGCAGGAAA	420
	GGTTCAGACC AGCCATCAAG TATTTTGGGG ATATTATTAG CGTGGGACAG AGATTGTTGC	480
	AAGGGGCCCG GATTTTAGGA ATTCCTGTTA TTGTAACAGA ACAATACCCT AAAGGTCTTG	540
10	GGAGCACGGT TCAAGAAATT GATTTAACAG GTGTAAACT GGTACTTCCA AAGACCAAGT	600
	TTTCAATGGT ATTACCAGAA GTAGAAGCGG CATTAGCAGA GATTCCCGGA GTCAGGAGTG	660
15	TTGTATTATT TGGAGTAGAA ACTCATGTGT GCATCCAACA AACTGCCCTG GAGCTAGTTG	720
	GCCGAGGAGT CGAGGTTTAC ATTGTTGCTG ATGCCACCTC ATCAAGAAGC ATGATGGACA	780
	GGATGTTTGC CCTCGAGCGT CTCGCTCRAR CCGGGATCAT AGTGACCACG AGTGAGGCTG	840
20	TTCTGCTTCA GCTGGTAGCT GATAAGGACC ATCCAAAATT CAAGGAAATT CAGAATCTAA	900
	TTAAGGCGAG TGCTCCAGAG TCGGGTCTGC TTTCCAAAGT ATAGGACATT TGAAGAACTG	960
25	GTATGCTACT CACTGGTGAA GGACAGTCAG GTGAAGGACT GTAAGCCAC ACAAGCTCTT	1020
	CTTATCTCTA CTAGAATTAA AATGTTAAGT CAAAAACGGC TCCTTTTTTG CGCCTCCTAG	1080
	TGAAACTTAA CCAGCTAGAC CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT	1140
30	CCGGTGCTGC TTACCTTCCT TTTTTGTAA TGTGCTTTTA TTTATTAAAA AAAATTACAA	1200
	TGAAGATGCC TGTTTTGTCT CTACTGTGTA CTCTGATCGT ATCTTTTCAA AGTGCAGACT	1260
35	CTTGTGAAGT TTTCTTAAAT TGTTCACMTT AAAGAAAATG ACGTACCAAC AATGATTGG	1320
	CTTTTATATT ACTGTAAGAT GTTATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG	1380
	ATTGATTGGA ATAAGATTAT TGCATATGAA TTTACCCACA GGA CTCTGAA TCATGTTACC	1440
40	CACTCCCTC ACAATGTTGT CCACCTTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT	1500
	GMTGAATAAT TACATATCTT TCTTGACTAT ACTGATTTCT TATTTTGGTC ACTATTACTA	1560
45	AATCTCTGTT AATATTCTCT CTTTAACTG AAAAGGGATG GGATAGAAGG GTTTGCAATG	1620
	CCATATTATT GGTGGAGGGC TGTTTTAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT	1680
	ACCAACATCT TGAATATATA TTCTAGTGTC CACAAGATT AGCAAAAAGA TAAAGCTTGG	1740
50	GTGGAATATC ATTTTAAAAT GTTCATGTTT TGTCTATAT TTTCTTCACC TACTCTCCAA	1800
	ATATTGTAAT GCAAAAAGTC TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAATGTT	1860
55	TCTCTTCGAT AAATTTATTT TCATTAAATA CTTRTTAGAG GGTTTTGAAA TGTTTTTCAA	1920
	ATAATGTAAT TGTGAACTG CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG	1980
	ATTGAAATTA TTTTGNCTC CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCTAAT	2040
60	ATTATTTTAA GGTNATAAAA TCTTGACATT TATAATCTTT C	2081

5 (2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 1717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

15 CCCCCGCGGA GCTGGACCCG CGGTGGGCTA GGGGCAGGGC CGGAGCCGCG GCGGCGGAGC 60
TGTGGATCCT TCATGATGAG AGATTGGGG ACACCTCTCT CTCCTGTGTG TAGTTGATAG 120
TTTGGTGGTG AAGAGATGGC TGACAGTGTC AAAACCTTTC TCCAGGACCT TGCCAGAGGA 180
20 ATCAAAGACT CCATCTGGGG TATTTGTACC ATCTCAAAGC TAGATGCTCG AATCCAGCAA 240
AAGAGAGAGG AGCAGCGTCG AAGAAGGGCA AGTAGTGTCT TGGCACAGAG AAGAGCCCG 300
25 AGTATAGAGC GGAAGCAAGA GAGTGAGCCA CGTATTGTTA GTAGAAATTT CCAGTGTTGT 360
GCTTGGAAATG GTGGAGTGTT CTGGTTCAGT CTCCTCTTGT TTTATCGAGT ATTTATTCCT 420
GTGCTTCAGT CGGTAACAGC CCGAATTATC GGTGACCCAT CACTACATGG AGATGTTTGG 480
30 TCGTGCGTGG AATTCTTCCT CACGTCAATT TTCAGTGCTC TTTGGGTGCT CCCCTTGTTT 540
GTGCTTAGCA AAGTGGTGAA TGCCATTTGG TTTGAGGATA TAGCTGACCT GGCATTTGAG 600
35 GTATCAGGGA GGAAGCCTCA CCCATTCCCT AGTGTCAGCA AAATAATTGC TGACATGCTC 660
TTCAACCTTT TGCTGCAGGC TCTTTTCCTC ATTCAGGGAA TGTTTGTGAG TCTCTTTCCC 720
ATCCATCTTG TCGGTCAGCT GGTAGTCTC CTGCATATGT CCCTTCTCTA CTCACTGTAC 780
40 TGCTTTGAAT ATCGTTGGTT CAATAAAGGA ATTGAAATGC ACCAGCGGTT GTCTAACATA 840
GAAAGGAATT GGCCTTACTA CTTTGGGTTT GGTMTGCCCT TGGCTTTTCT CACAGCAATG 900
45 CAGTCCTCAT ATATTATCAG TGGCTGCCTT TTCTCTATCC TCTTTCCCTT ATTCATTATC 960
AGCGCCAATG AAGCAAAGAC CCCTGGCAAA GCRTATCTCT TCCAGTTGCG CCTCTTCTCC 1020
TTGGTGGTCT TCTTAAGCAA CAGACTCTTC CACAAGACAG TCTACCTGCA GTCGGCCCTG 1080
50 AGCAGCTCTA CTTCTGCAGA GAAGTTCCTC TCACCGCATC CGTCGCCTGC CAAACTGAAG 1140
GCTACTGCAG GTCACTGAGT TGCCTGCCAT CCAAAGGGGA TGGGCGGGAT TGGAAGAAGC 1200
55 TGTGGCAGCT CTTTTCCTCG TTCACCTCCC GCCTGCCAGG GAAGGCAGGA CCCGCTCTGC 1260
CAAGGGCCCT CTGCGTATTC CCTTCTCTCT GAGGAATTGA AATTTTGTG TCTGGTGAC 1320
GTAAGGCAGA ATGTTCCCTG ACACCAAGTG GTGGATTTTT AACATCACCG TGAGTCTGAA 1380
60

AGGACCACAG GTTTTCTGCG AGCTATTTTC TAGCATTTGC CAGTCCCTGT GCCTGGAAGT 1440
ATTGGAACAC TTTGTMTTTC TCCCTGTGCC ATTTACCCCTT CCACCTTTCC ATCCTGCCTT 1500
5 CTACCACCCT TGGATGAATG GATTTTGTA TTTAGCTGT TGTATTTTGT GAATTTGTTA 1560
ATTTTGTGT TTTTCTGTGA AACACATACA TTGGATATGG GAGGTAAAGG AGTGTCCAG 1620
TTGCTCCTGG TCACTCCCTT TATAGCCATT ACTGTCTTGT TTCTGTAAAC TCAGGTTAGG 1680
10 TTTTGGTCTC TCTTGCTCCA CTGCAAAAAA AAAAAA 1717

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(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

25

CCACGCGTCC GGTCACTATG TAGTGGAGGG GCAGACACCC TCCCGCAAAT TCTGGAAGGT 60
TCTTAGTCTC GACTAGGCA GTAGCCCAG GACTCCTAGT CGCCGGCTTC AGGTCACTGC 120
30 CGGCTGAACG GAGCTGCCGT CGCCATGTTT GGCTGCTTGG TGGCGGGGAG GCTGGTGCAA 180
ACAGCTGCAC AGCAAGTGGC AGAGGATAAA TTTGTMTTTC ACTTACCTGA TTATGAAAGT 240
ATCAACCATG TTGTGGTMTT TATGCTGGGA ACAATCCCAT TTCCTGAGGG AATGGGAGGA 300
35 TCTGTCTACT TTTCTTATCC TGATTCAAAT GGAATGCCAG TATGGCAACT CCTAGGATTT 360
GTCACGAATG GGAAGCCAAG TGCCATCTTC AAAATTTTCTG GTCTTAAATC TGGAGAAGGA 420
40 AGCCAACATC CTTTGGAGC CATGAATATT GTCCGAATC CATCTGTTGC TCAGATTGGA 480
ATTTCACTGG AATTATTAGA CAGTATGGCT CAGCAGACTC CTGTAGGTAA TGCTGCTGTA 540
TCCTCAGTTG ACTCATTAC TCAGTTCACA CAAAAGATGT TGGACAATTT CTACAATTTT 600
45 GCTTCATCAT TTGCTGTCTC TCAGGCCAG ATGACACCAA GCCCATCTGA AATGTTTATT 660
CCGGCAAATG TGGTCTGAA ATGGTATGAA AACTTTCAA GACGACTAGC ACAGAACCTT 720
50 NTNTTTTGGN AACATAATT TGAATAAAAT AATTTTAAAT GGATTNTGNA AAAAAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAA 804

55

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GGCACAGCCC AGGGCCTTGA AGCCAGCTGG CCTTGGAGAG GGGCTGCTGT GCCAGCTTGG 60
GGAGGGTCTG GGATGGGGCT GCCCTGATG GCCCTGATGT GGAGTACCTT GCCAGCATCT 120
10 GCTGGGGTGA ACTTTATTTT AGCCCTTCCC TTGTGCTCT TATGGAAGAA CAGAGGAGGG 180
GTGGGCAGGT CAGTGATGTC AGCAGTGGAG TGATTTCCAG CACAGCGGCT TCTGGGAAGA 240
15 GGGCATGGAG GCATTTCTTT CAGGGAAATG GTCCATNATT TCAGCCAGAA GGCATTGCAT 300
TAAGTTAAGT CCNGGACTTT TGTGGCCAG CTCTGTGTTA TTAAGGGCCC TTGGCGAAGA 360
CTTCAAGGAG GGGGCAAAAN GACCTTTAAG TTTTtaggTT TAACACAGGG AACCNCNAAA 420
20 GGGTTATTTT G 431

25

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 3752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

35 NGGCACGAGG AGAGTCACCT GGA CTAGAGATAT CCAATGACCC AGACAAAATT 60
AAACTTCAGC TTTCTAAGCA TAAGGAGTTT CAGAAGACTC TTGGTGGCAA GCAGCCTGTG 120
40 TATGATACCA CAATTAGAAC TGGCAGAGCA CTGAAAGAAA AGACTTTGCT TCCCGAAGAT 180
ASTCAGAAAC TTGACAATTT CCTAGGAGAA GTCAGAGACA AATGGGATAC TGTTTGTGGC 240
AAGTCTGTGG AGCGGCAGCA CAAGTTGGAG GAAGCCCTGC TCTTTTCGGG TCAGTTCATG 300
45 GATGCTTTGC AGGCATTGGT TGA CTGTTA TACAAGGTGG AGCCACAGCT GGCTGAGGAC 360
CAGCCCGTGC ACGGGGGACC TTGACCTCGT CATGAACCTC ATGGATGCAC ACAAGGTTTT 420
50 CCAGAAGGAA CTGGNGAAAG CGAACAGGAA CCGTTCAGGT CCTGAAGCGG TCAGGCCGAG 480
AGCTGATTGA GAATAGTCGA GATGACACCA CTTGGGTAAA AGGACAGCTC CAGGAACTGA 540
GCACTCGCTG GGACACTGTC TGTAACTCT CTGTTTCCAA ACAAAGCCGG CTTGAGCAGG 600
55 CCTTAAACA ACCGGAAGTG TTTGAGACA CAGTCCACAT GCTGTTGGAG TGGCTTCTG 660
AAGCAGAGCA AACGCTTCGC TTTGGGGAG CACTTCCTGG ATGACACAGA GGCCCTGCAG 720
60 TCTCTATTG ACACCCATAA GGAATTCATG AAGAAAGTAG AAGAAAAGCG AGTGGACGTT 780

	AACTCAGCAG TAGCCATGGG AGAAGTCATC CTGGCTGTCT GCCACCCCGA TTGCATCACA	840
	ACCATCAAAC ACTGGATCAC CATCATCCGA GCTCGCTTCG AGGAGGTCCT GACATGGGCT	900
5	AAGCAGCACC AGCAGCGTCT TGAAACGGCC TTGTGAGAAC TGGTGGCTAA TGCTGAGCTC	960
	CTGGAAGAAC TTCTGGCATG GATCCAGTGG GCTGAGACCA CCCTCATTCA GCGGGATCAG	1020
10	GAGCCAATCC CGCAGAACAT TGACCGAGTT AAAGCCCTTA TCGCTGAGCA TCAGACATTT	1080
	ATGGAGGAGA TGACTCGCAA ACAGCCTGAC GTGGACCGGG TCACCAAGAC ATACAAAAGG	1140
	AAAAACATAG AGCCTACTCA CGCGCCTTTC ATAGAGAAAT CCCGCAGCGG AGGCAGGAAA	1200
15	TCCCTAAGTC AGCCAACCCC TCCTCCCATG CCAATCCTTT CACAGTCTGA AGCAAAAAAC	1260
	CCACGGATCA ACCAGCTTTC TGCCCGCTGG CAGCAGGTGT GGCTGTTAGC ACTGGAGCGG	1320
20	CAAAGGAAAC TGAATGATGC CTTGGATCGG CTGGAGGAGT TGAAAGAATT TGCCAACTTT	1380
	GACTTTGATG TCTGGAGGAA AAAGTATATG CGTTGGATGA ATCACA AAAA GTCTCGAGTG	1440
	ATGGATTTC TCCGGCGCAT TGATAAGGAC CAGGATGGGA AGATAACAG TCAGGAGTTT	1500
25	ATCGATGGCA TTTTAGCATC CAAGTCCCC ACCACCAAGT TAGAGATGAC TGCTGTGGCT	1560
	GACATTTTCG ACCGAGATGG GGATGGTTAC ATTGATTATT ATGAATTTGT GGCTGCTCTT	1620
30	CATCCCAACA AGGATGCGTA TCGACCAACA ACCGATGCAG ATAAAATCGA AGATGAGGTT	1680
	ACAAGACAAG TGGCTCAGTG CAAATGTGCA AAAAGGTTTC AGGTGGAGCA GATCGGAGAG	1740
	AATAAATACC GGTTCCTCCT CGGCAATCAG TTTGGGGATT CTCAGCAGTT GCGGCTGGTC	1800
35	CGTATTCTGC GCAACCGTGA TGGTTCGCGT TGGTGGAGGA TGGATGGCCT TGGATGAATT	1860
	TTTAGTGAAA AATGATCCCT GCCGAGCAG AGGTAGA ACT AACATTGAAC TTAGAGAGAA	1920
40	ATTATCCTTA CCAGAGGGAG CATCCCAGGG AATGACCCCC TTCCGCTCAC GGGGTCGAAG	1980
	GTCCAAACCA TCTTCCGGG CAGCTTCCCC TACTCGTTCC AGCTCCAGTG CTAGTCAGAG	2040
	TAACCACAGC TGTACATCCA TGCCATCTTC TCCAGCCACC CCAGCCAGTG GAACCAAGGT	2100
45	TATCCCATCA TCAGGTAGCA AGTTGAAACG ACCAACACCA ACTTTTCATT CTAGTCGGAC	2160
	ATCCCTTGCT GGTGATACCA GCAATNAGTT CTTCCCCGGC CTCCACAGGT GCCAAACTA	2220
50	ATCGGGCAGA CCCTAAAAAG TCTGCCAGTC GCCCTGGGAG TCGGCTGGG AGTCGAGCCG	2280
	GGAGTCGAGC CAGCAGCGG CGAGGAAGTG ACGCTTCTGA CTTTGACCTC TTAGAGACGC	2340
	ATTGCTTGTT CCGACACTTC AGAAAGCAGC GCTGCAGGGG GCCAAGGCAA CTCCAGGAGA	2400
55	GGGCTAAACA AACCTTCCAA AATCCCAACC ATGTCTAAGA AGACCACCAC TGCCTCCCCC	2460
	AGGACTCCAG GTCCCAAGCG ATAACACTGT CTAAGCACC CCAAGCCACT ATCCACTTTG	2520
60	AATCCTGCTC CATACATGG GTGTATATTT ATTCTGAACG GGAGAAGTTA TATTGTTAAA	2580

5 AGTGTAAGAG AATAATTGTG TTATGAAGCT GCCTTATTTT TTTCTTTTTT GTAAGTTACT 2640
 ATTTTCATGT GAATATTTAT GTAGATAAAA TTGCGCTCCT GGTAACCCCTG TAATGGATGG 2700
 GGGCCAGAAA TGAAATATTT GAGAAAAACA AGTGAAAAGG TCAAGATACA AATGTGTATT 2760
 AAAAAAAAAA AAGCCTATTA ATAGGGTTTC TCGCGGTGTC AGGGTTGTAA ACCTGCTTTA 2820
 10 TCTTTTAGGA TTATTCCTAA ATGCATCTTC TTTATAAACT TGACTTGCTA TCTCAGCAAG 2880
 ATAAATTATA TTAAAAAAT AAGAATCCTG CAGTGTTTAA GGAACCTTTT TTTTGTAAT 2940
 CACGGACACC TCAATTAGCA AGAACTGAGG GGAGGGCTTT TTCCATGTGT TAATGTTTTG 3000
 15 TGATTTTAGA CTAAAGAGAG GGAACCTCAT CTAAGTAACA TTTGCACATG ATACAGCAAA 3060
 AGGAGTTCAT TGCAATACTG TCTTTGGATA TTGTTTCAGT ACTGGGTGTT TAAAGGACAA 3120
 20 ATAGCTGCTA GAATTCAGGG GTAAATGTAA GTGTTGAGAA AACGTCAGAA CATTGCGGT 3180
 TTTAACTGA TTTGTTGCTC CCTATCCAGC CTAGACACCA GAACTCTTG TGTTCACCAG 3240
 GACCCAGACC CTGGCAAGG GATAGGCTCG TTGGTGACAT TGTGAATTC AGATTGTTT 3300
 25 TATCCACTTT TTTTGCTATT TATTTAAATG GTCGATCAAC TTCCACAAA CTGAGGAATG 3360
 AATTCCACGA GCCTGTCTG AAAATGTGGA CGTAAGACAA ACACGTGCTC GTCCTTTAAT 3420
 30 GGAGTTCACC AGCACACTTG TTAACCAGTC CTGTTGCTT TCGTCTTTTT TTGTGCGTAA 3480
 TAAAGTCAAC TGACCAAGTG ACCATGAAAA GGGGCTGTCT GGGGCTCCTG TTTTTTAGCT 3540
 GCTGTTCTTC AGCTCCGACC ATGTTGCTGT GTGATTATCT CAATTGGTTT TAATTGAGGC 3600
 35 AGAACTGAA GCTCTACCA TGAAGTGTG AGAAACAAGA CACACTTTTG TATTAAAATT 3660
 GCTTGCACTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGG GGGGCCCGGT 3720
 40 ACCCAATTCTG CCGTATATGA TCGTAAACAA TC 3752

45 (2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

55 TGACCCCTCTG CCGCGCGGC TCAGTGCTGG ACGCTTTCTG TTTTGTGCA GTCGGTCTC 60
 GGTAACACCA GCGGCCTGTG GTCCACCACT CCATTGAGCA GCTCCATTTG GTCCAGCAAC 120
 CTTAGCAGCG CCTTCCCTTC ACCACTCCAG CAAACACGCT GGCAAGCATC GGCCTCATGG 180
 60

	GCACAGAAAA CTCCCCTGCT CCTCACGCTC CCTCCACCTC CAGTCCAGCT GACGACTTGG	240
	GACAGACCTA CAACCCGTGG CGGATATGGA GCCCCACGAT TGGAGAAGA AGCTCGGACC	300
5	CTTGGTCTAA TTCGCACTTT CCTCACGAGA ATTAAATTAA GCAAAAAACA AACAAACATA	360
	GTGGGCCCTC GTCTAGATCA TGATGTGCCA GTTCTGAGA CATCTTTTAA AGGCTCTTAC	420
10	TGCAGCTCCC CTCCCCACCC TCCTCTTCTT TGCAAAACAG ACCCAAGCAG GGCAGGCTCA	480
	GACCACTCGC TTCTTTCAGA TCTTCTTGC AATTATGATA ACATGAGATT TGCTGTTGTG	540
	CTTTTAGAGA AAAGTCTGGA CTCAGCCACA AACTCTAATA AGACCTGTAC ATCTGAGAAC	600
15	CTTTCCCGTT ACTGCGTTTT CACCACCTGT CTTCCCATG CTTTATTTAT CTGTATGAAC	660
	ACAGATTTGA CATTACAGCT AAGGAAATAA TTTGAGTTGA TTCAGAAATC CTGGCATGTG	720
20	ACAATTTTGT TAAATTACCA AGTTTGTTTT TTAATAATTT CTCAATATTA TCGCCAAGA	780
	TCTAATTTTA AAAGTGTATG AGGACTTTGT GCTGAAAATA GAGTATTTTT TTAAAGTAAG	840
	GCTGTCTTGG TTTAAAAGCA GATTACAGAA ATGTAAGTCA ACTTAAGAAC RGTGAATGAA	900
25	TGTAAAAACA TTCAGTYGAG ACCATATGCA TTTTCTGTGC TGTGTGTACT TGAGGTATGT	960
	AACATTTGTA TACCTGAAC TATTTTAAAG ATGAACTGAA ATGCACATAG CCAAGTCTTG	1020
30	AGATACAAGA TTGAATGTGT ATTTCTTAAA AATACAACCT TGTGTGTAC TTTGAAATAA	1080
	ATGATGCTTT TTTCAAAAAA AAAAAAAAAA AAAAAAAC TCGAGGGGGG GCCCGGTACC	1140
	CAAT	1144

35

(2) INFORMATION FOR SEQ ID NO: 129:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1830 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

	GCATGCAGAG GAGCACCCCTG AGCGTGTGCC TGGAGCAGGC GGCCATSTTG GCACGGAGCC	60
50	ACGGGTTGCT GCCCAAGTGC ATCATGCAGG CCACGGACAT CATGCGGAAC AGGGCCCAAG	120
	GGTGGAGATT CTGGCCAAAA ACCTGCGAGT CAAGGACCAG ATGCCCCAGG GTGCTCCGCG	180
55	CCTCTACCGC CTCTGCCAGC CGCCGGTGGG TGGGGACCTC TGAACACCCA AATGCCCCAC	240
	GCTGGGCCGC GGCCTCTGGA GCTGGGATTT GGGAGGACAC AGCAGGCAGC GCTGGCCTTC	300
	TCCAGGGATG GCCCAANGCT TCCGCARCCG CCCGTTCCGG GACCTGCCCA GCGTCTCTCC	360
60	TGCCTCCTTC CGGGACAAGC CTGGCCACCC TCGCTGTGAT GACGAGCTGG CTGATTGGCC	420

	CTGGGCCCGC CCATTCTTCA CACGCCTGCC AGAAGCTGGA GGGGTGCTGG AGACCCATAG	480
5	AGCTGATGGG AGCAGCTGGT GCCTGGCCTT CGGCTCCTGC GTCCCCAGAA CCCAAGGGAA	540
	CGTCATGGAG GCCACATGGG GCCACCCGGC TCCCTCGGGA TGGCTCCGCT GCACTTTGA	600
	AACCCCGGTT TCCTTCAACG TCCACATTCC AGGTGACCAC ACGTGTCTCC TCCTCCTCAT	660
10	CTTAGCTTCC AGGTTACCCC TAACCCTGTA CTAACCTGCT TGGTGGACTT GGAAAAGACT	720
	TGGCTCTGTC GGGAAAGGAG AGACGGGGCC TCCATCACGC CTGTTACCAG AGGATCCCCG	780
15	AGAGCCACAC CAGCTCTGGA CATCACCGCC CCTGGAAC TG GCCACCAG CCCTGGGCAC	840
	GAGATTGCT CTGACTTTAT TTATATGGCA TGAAATCTCT GGTTTATTTT GGGATTTT	900
	GTGTGTGGTG TTGTCAAAGT TTGTMTTTC TAAAGTTGTG TGATTATATA TTTGACATTT	960
20	TACATTTCAA AGAAAGGTAT GTTGTCTAAC AGGGGACCAA CAGAAGGTAG TATTGACAAC	1020
	TGTTCTGCT TCTACTAAAA AAAAAAGAGC AAAAAAGAAA AACTAAATTA TTGAAAAATT	1080
25	AAAAAATGTC ATTGTTTCTT GTTGTTAAT ATTAGGGTTG TAAGGTGTCG TTTTGAGGTA	1140
	TCGACTGTGA TTCTTCCCC CACCCTCCAT TCTCCAGCGG TTGGCCGGTG TTAGAAGTCG	1200
	CTCTCTTTGA GTGACTGGCT ACAAGGGCCT GAGAGGTGGC CAGCCAGGGT TGGAGCTGGA	1260
30	GGGATGGAG CCCACCTGA GGTGCCGTGT CACACGGGTT AGAGGGTCAC TGGGAAACAC	1320
	CGGGCGGTGG CTTCTGTGAT TTATTTTCTT GATGGTAACT TCTCAGAGCA GGGCRATTGG	1380
35	GACATACCA GCCAGAGCAC AGGAAGCCAC CCTGCCTGCT GGGGAGGAGG GACCCACACA	1440
	AGCCCCCTCG GCAGTTTGTG CCCCCAGCTT CGGTATGCCT TCAGGGAAAG GTCACAGCTG	1500
	GGGAGGAAGC GGGGGGACGC CTGTCACCCC TGGCAGGTGG TGAGTTCAGG TGGGGGCTCC	1560
40	CTGCTKCCCC CAGGCCTGGG AGCTTGAAGC CCTCCCGGCA TCTGGCATCC GAGCCTCCCG	1620
	CCCTCCAGGG TGCCTTCCC TCTCTTGCCG CAGCATACAC GAGGGCAGGC AGTGGCCTTG	1680
45	TCAGTGTATC TTGCATCAGA GACAAAGGAG GACCCGCTTT AGCCCTGCTG CGGGAAATGG	1740
	GGGATGGCCC AGGGCCAGCG CATTTGTCAC TGGTTTACTT TAAAATGTAC AGATTCTTCT	1800
50	CGTTAAATTC TTGATAGATT TTTTATTATT	1830

(2) INFORMATION FOR SEQ ID NO: 130:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

	GGCCGCCCGG ATGGCGACCC CAGCCTCGGC CCCAGACACA CGGGCTCTGG TGGCAGACTT	60
5	TGTAGGTTAT AAGCTGAGGC AGAAGGGTTA TGTCTGTGGA GCTGGCCCCG GGGAGGGCCC	120
	AGCAGCTGAC CCGCTGCACC AAGCCATGCG GGCAGCKGGA GATGAGTTCC AGACCCGCTT	180
10	CCGGCGCACC TTCTCTGATC TGGCGGCTCA GCTGCATGTG ACCCCAGGCT CAGCCCAACA	240
	ACGCTTCACC CAGGTCTCCG ATGAACCTTT TCAAGGGGGC CCCAACTGGG GCCGCCTTGT	300
	AGCCTTCTTT GTCTTTGGGG CTGCACTGTG TGCTGAGAGT GTCAACAAGG AGATGGAACC	360
15	ACTGGTGGGA CAAGTGCAGG AGTGGATGGT GGCCTACCTG GAGACGGGC TGGCTGACTG	420
	GATCCACAGC AGTGGGGGCT GGTATATCCCA GATCACTGAA GCTGAGATGG CTGATGAAGT	480
20	AATTTGCAGT GAAATTTTAA GCGACTGTGA CTCTGCTGCA AGTTCCCCAG ATCTTGAGGA	540
	GCTGGAAGCT ATCAAAGCTC GAGTCAGGGA GATGGAGGAA GAAGCTGAGA AGCTAAAGGA	600
	GCTACAGAAC GAGGTAGAGA AGCAGATGAA TATGAGTCCA CCTCCAGGCA ATGCTGGCCC	660
25	GGTGATCATG TCCATTGAGG AGAAGATGGA GGCTGATGCC CGTTCCATCT ATGTTGGCAA	720
	TGTGGACTAT GGTGCAACAG CAGAAGAGCT GGAAGCTCAC TTTCATGGCT GTGGTTCAGT	780
30	CAACCGTGT ACCATACTGT GTGACAAATT TAGTGGCCAT CCCAAAGGGT TTGCGTATAT	840
	AGAGTTCTCA GACAAAGAGT CAGTGAGGAC TTCTTGGCC TTAGATGAGT CCCTATTTAG	900
	AGGAAGGCAA ATCAAGGTGA TCCCAAAACG AACCAACAGA CCAGGCATCA GCACAACAGA	960
35	CCGGGGTTTT CCACGAGCCC GCTACCGCGC CCGGACCACC AACTACAACA GCTCCCGCTC	1020
	TCGATTCTAC AGTGGTTTTA ACAGCAGGCC CCGGGTCCG GTCTACAGG GCCGGGCTAG	1080
40	AGCGACATCA TGGTATTCCT CTACTAAAA AAAGTGTGTA TTAGGAGGAG AGAGAGGAAA	1140
	AAAAGAGGAA AGAAGGAAAA AAAAAAGAAT TAAAAAATAA AAAAAAATAA ACAGAAGWTG	1200
	MCCTTGATGG AAAAAAATA TTTTTTAAAA AAAAGATATA CTGTGGAAGG GGGGAGAATC	1260
45	CCATAACTAA CTGCTGAGGA GGGACCTGCT TTGGGGAGTA GGGGAAGGCC CAGGGARTGG	1320
	GGCAGGGGGC TGCTTATTC ACTGCGGGAT TCGCCATGGA CACGTCTCAA CTGCGCAACT	1380
50	GCTTGCCCAT GTTTCCTTGC CCCACCCAC CCCTCTTCTC CGGCTCCCTG CCCCTCCAGA	1440
	TTGCCTGGTG ATCTATTTTG TTTCCTTTTG TGTTCCTTTT TCTGTTTGA GTGTCTTTCT	1500
	TTGCAGGTTT CTGTAGCCCG AAGATCTCCG TTCCGCTCCC AGCGGCTCCA GTGTAAATTC	1560
55	CCCTTCCCCC TGGGGAAATG CACTACCTTG TTTTGGGGG TTTAGGGTG TTTTGTTTT	1620
	TCAGTTGTTT TGTTTTTTTG TTTTTTTT TTTCTTTTGC CTTTTTTCCC TTTTATTTGG	1680
60	AGGGAATGGG AGGAAGTGGG AACAGGGAGG TGGGAGGTGG ATTTTGTTTA TTTTTTTAGC	1740

TCATTTCCAG GGGTGGGAAT TTTTTTTTAA TATGTGTCAT GAATAAAGTT GTTTTGTAAA 1800
AKAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1860
5 AAAA 1864

10 (2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2041 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

20 GGCACGAGCG CGCGGCAGGG CCCTGGACCC GCGCGGCTCC CGGGGATGGT GAGCAAGGCG 60
CTGCTGCGCC TCGTGTCTGC CGTCAACCGC AGGAGGATGA AGCTGCTGCT GGGCATCGCC 120
TTGCTGGCCT ACGTCGCCTC TGTMTGGGGC AACTTCGTTA ATATGAGGTC TATCCAGGAA 180
25 AATGGTGAAC TAAAAATTGA AAGCAAGATT GAAGAGATGG TTGAACCACT AAGAGAGAAA 240
ATCAGAGATT TAGAAAAAAG CTTTACCCAG AAATACCCAC CAGTAAAGTT TTTATCAGAA 300
30 AAGGATCGGA AAAGAATTTT GATAACAGGA GCGCAGGGT TCGTGGGCTC CCATCTAACT 360
GACAACTCA TGATGGACGG CCACGAGGTG ACCGTGGTGG ACAATTCTTT CACGGGCAGG 420
AAGAGAAACG TGGAGCACTG GATCGGACAT GAGAACTTCG AGTTGATTAA CCACGACGTG 480
35 TGGAGCCCCT CTACATCGAG GTTGACCAGA TATACCATCT GGCATCTCCA GCCTCCCCCTC 540
CAAACCTACAT GTATAATCCT ATCAAGACAT TAAAGACCAA TACGATTGGG ACATTAAACA 600
40 TGTMTGGGCT GGCAAAACGA GTCGGTGGCC GTCTGCTCCT GGCTCCACA TCGGAGGTGT 660
ATGGAGATCC TGAAGTCCAC CCTCAAAGTG AGGATTACTG GGGCCACGTG AATCCAATAG 720
GACCTCGGGC CTGCTACGAT GAAGGCAAAC GTGTGTCAGA GACCATGTGC TATGCCTACA 780
45 TGAAGCAGGA AGGCGTGGAA GTGCGAGTGG CCAGAATCTT CAACACCTTT GGGCCACGCA 840
TGCACATGAA CGATGGGCGA GTAGTCAGCA ACTTCATCCT GCAGGCGCTC CAGGGGGAGC 900
50 CACTCACGGT ATACGGATCC GGGTCTCAGA CAAGGGCGTT CCAGTACGTC AGCGATCTAG 960
TGAATGGCCT CGTGGCTCTC ATGAACAGCA ACGTCAGCAG CCCGGTCAAC CTGGGGAACC 1020
CAGAAGAACA CACAATCCTA GAATTTGCTC AGTTAATTAA AAACCTTGTT GGTAGCGGAA 1080
55 GTGAAATTCA GTTCTCTCTC GAAGCCCAGG ATGACCCACA GAAAAGAAAA CCAGACATCA 1140
AAAAAGCAAA GCTGATGCTG GGGTGGGAGC CCGTGGTCCC GCTGGAGGAA GGTTTAAACA 1200
60 AAGCAATTCA CTACTCCGT AAAGAACTCG AGTACCAGGC AAATAATCAG TACATCCCCA 1260

5 AACCAGAGCC TGCCAGAATA AAGAAAGGAC GGAATCGCCA CAGCTGAACT CCTCACTTTT 1320
 AGGACACAAG ACTACCATTG TACACTTGAT GGGATGTATT TTTGGCTTTT TTTTGTGTGTC 1380
 GTTTAAAGAA AGACTTTTAA AGGTGTCATG AAGAACAAAC TGAATTTTCA TTCTGAAGCT 1440
 TGCTTTAATG AAATGGATGT GCCTAAAAGC TCCCTCAAA AACTGCAGA TTTTGCCTTG 1500
 10 CACTTTTGA ATCTCTCTTT TTATGTAAAA TAGCGTAGAT GCATCTCTGC GTATTTTCAA 1560
 GTTTTTTAT CTGTCTGTGA GAGCATATGT TGTGACTGTC GTTGACAGTT TTATTTACTG 1620
 GTTCTTTGT GAAGCTGAAA AGGAACATTA AGCGGGACAA AAAATGCCGA TTTTATTTAT 1680
 15 AAAAGTGGT ACTTAATAAA TGAGTCGTTA TACTATGCAT AAAGAAAAAT CCTAGCAGTA 1740
 TTGTCAGGTG GTGGTGCGCC GGCATTGATT TTAGGCAGA TAAAGAATT CTGTGTGAGA 1800
 20 GCTTTATGTT TCTCTTTTAA TTCAGAGTTT TTCCAAGGTC TACTTTTGAG TTGCAAACTT 1860
 GACTTTGAAA TATTCCTGTT GGTCAATGATC AAGGATATTT GAAATCACTA CTGTGTTTGT 1920
 CTGCGTATCT GGGCGGGGG CAGGTGGGG GGCACAAAGT TAACATATTC TTGGTTAACC 1980
 25 ATGGTTAAAT ATGCTATTTT AATAAAATAT TGAACTCAC CAAAAAATAA AAAAAAATAA 2040
 A 2041

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(2) INFORMATION FOR SEQ ID NO: 132:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2012 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

TACCAAGCTG CAAGAATCTA CTATATCATG GCAGAAGAAG TAGAGTGGGA CTATTGCCCT 60
 45 GACCGGAGCT GGGAACGGGA ATGGCACAAC CAGTCTGAGA AGGACAGTTA TGGTTACATT 120
 TTCCTGAGCA ACAAGGATGG GCTCCTGGGT TCCAGATACA AGAAAGCTGT ATTCAGGGAA 180
 TACACTGATG GTACATTGAG GATCCCTCGG CCAAGGACTG GACCAGAAGA AACTTGGGA 240
 50 ATCTTGGGTC CACTTATCAA AGGTGAAGTT GGTGATATCC TGAATGTGGT ATTCAAGAAT 300
 AATGCCAGCC GCCCCTACTC TGTGCATGCT CATGGAGTGC TAGAATCTAC TACTGTCTGG 360
 55 CCACTGGCTG CTGAGCCTGG TGAGGTGGTC ACTTATCAGT GGAACATCCC AGAGAGGTCT 420
 GGCCCTGGGC CAATGACTCT GCTGTGTTT CCTGGATCTA TTATTTCTGCA GTGGATCCCA 480
 TCAAGGACAT GTATAGTGGC CTGGTGGGG CCTTGGCTAT CTGCCAAAAG GGCATCCTGG 540
 60

	NAGCCCCATG GAGGACGGAN TGACATGGAT CGGGAATTTG CATTGTTGTT CTMGATTTT	600
	GATGAAAATA AGTCTTGGTA TTTGGAGGAA AATGTGGCAA CCCATGGGTC CCAGGATCCA	660
5	GGCAGTATTA ACCTACAGGA TGAACTTTTC TTGGAGAGCA ATAAAATGCA TGCAATCAAT	720
	GGGAAACTCT ATGCCAACCT TAGGGGTCTT ACCATGTACC AAGGAGAACG AGTGGCCTGG	780
	TACATGCTGG CCATGGGCCA AGATGTGGAT CTACACACCA TCCACTTTCA TGCAGAGAGC	840
10	TTCTCTATC GGAATGGCGA GAACTACCGG GCAGATGTGG TGGATCTGTT CCCAGGGACT	900
	TTTGAGGTTG TGGAGATGGT GGCCAGCAAC CCTGGGACAT GGCTGATGCA CTGCCATGTG	960
15	ACTGACCATG TCCATGCTGG CATGGAGACC CTCTTCACTG TTTTCTCTCG AACAGAACAC	1020
	TTAAGCCCTC TCACCGTCAT CACCAAAGAG ACTGAAAAAG CAGTGCCCCC CAGAGACATT	1080
	GAAGAAGGCA ATGTGAAGAT GCTGGGCATG CAGATCCCCA TAAAGAATGT TGAGATGCTG	1140
20	GCCTCTGTTT TGGTTGCCAT TAGTGTCAAC CTTCTGCTCG TTGTTCTGGC TCTTGGTGGA	1200
	GTGGTTTGGT ACCAACATCG ACAGAGAAAG CTACGACGCA ATAGGAGGTC CATCCTGGAT	1260
25	GACAGCTTCA AGCTTCTGTC TTTCAAACAG TAACATCTGG AGCCTGGAGA TATCCTCAGG	1320
	AAGCACATCT GTAGTGCACCT CCCAGCAGGC CATGGACTAG TCACTAACCC CACACTCAAA	1380
	GGGGCATGGG TGGTGGAGAA GCAGAAGGAG CAATCAAGCT TATCTGGATA TTTCTTTCTT	1440
30	TATTTATTTT ACATGGAAAT AATATGATTT CACTTTTCTT TTAGTTTCTT TGCTCTACGT	1500
	GGGCACCTGG CACTAAGGGA GTACCTTATT ATCCTACATC GCAAATTTCA ACAGCTACAT	1560
35	TATATTTCTT TCTGACACTT GGAAGGTATT GAAATTTCTA GAAATGTATC CTTCTCACAA	1620
	AGTAGAGACC AAGAGAAAAA CTCATTGATT GGGTTTCTAC TTCTTTCAAG GACTCAGGAA	1680
	ATTTCACTTT GAACTGAGGC CAAGTGAGCT GTTAAGATAA CCCACACTTA AACTAAAGGC	1740
40	TAAGAATATA GGCTTGATGG GAAATTGAAG GTAGGCTGAG TATTGGGAAT CCAAATTGAA	1800
	TTTGTATCTT CCTTGGCAGT GAACTACTTT GAAGAAGTGG TCAATGGGTT GTTGCTGCCA	1860
45	TGAGCATGTA CAACCTCTGG AGCTAGAAGC TCCTCAGGAA AGCCAGTTCT CCAAGTTCTT	1920
	AACCTGTGGC ACTGAAAGGA ATGTTGAGTT ACCTCTTCAT GTTTTAGACA GCAAACCCTA	1980
	TCCATTAAAG TACTTGTTAG AACACTGAAA AA	2012
50		

55 (2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1669 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

5	GAGCAGTATT TTAACCAACT TGTATTACAG ATGTTACAGT TCATGTTAGG AAGTCAGAAA	60
	AGACTTTGTT TGTCTTTGTT CTGCTGATGT GAGTCATGTT TTGTGGGGTC TTCCATGGCA	120
	CATTTACCTG TTGCTCCGTC CAGATGTTGA GGGCCAGTCT AGGCTGACAC ATCCTACCCG	180
10	AGGACAAGCC TGTTCCTCCAT TTCTTCACTC TCCCCTCCCC ATATAGCAAC TCTCCCAGGT	240
	TTAGATTACC GTTTTCGACG ACAGATTAAC CAAAAATGCC CCACACAGGT TTTATTACTG	300
	TTATATACTA TACTTTTAAAC AGTACAGACC CTAAATTTTA TTATTGTGTG CTCCCCCAAT	360
15	CTGATACCAA ATGTTTAAAG TTGTTTGAAA TCCAAACATG GTAGTGTTC A TGGGTAAATA	420
	TTTTCTAGGC TATGTAAGAG TTAGCAGCCC ATAGCATAGA AGTAATCAAG TAGCATCTGA	480
20	GACTGTTGGA GGCCTAGGG CCTCTCTGGG CCTAACAGCC TCACTTCCCC AGCCTCACCT	540
	TGCTGTCTC TGACACTGCC ATCAGGGCTG TTAGTGGCAC CTGTATGAGG CCAAGTGTGC	600
	GTCCAGGGGA ACAGCACAGG TTAATGCGTC TCCCTAGAAC TCATGAAGTC AGTTTAATTC	660
25	ATGCATGAAC ATGAGTTCAT TTTATGTTTT ATATAGCTTT CTTAGACATA CCAAACCATC	720
	ATTCATAAAT CAGATAAATT ATTCACTTTT TGTGTTTAGA AAGCTAAGTA TGTGTAGCTG	780
30	GAAACAAAAA TGAGCGTGT TCTCTCCTG TTAATCTAGA GTGTGCAGT ACACATGTGT	840
	GGATAATTTT ATGTTCCAGG GCGCTTGCC ATCTCCCATG GACTGATTCC CAGGAAGAAA	900
	AGCCCAAAGG GAAACCCACG ATTCTTTTCG AGTAGATGTG GGAAAGAGCC CATGAGGGA	960
35	TATGAGGTCC TGTGAAATTC AGTTGTGTGT GTGGCTCCTT GTTAGCAGTC ATGTTGACAT	1020
	GGTGTTAGGA GGCTCCCCAT CCACCCTTTA CATGATGTAG GGACCAGTGT CTTGTGAGAT	1080
40	TAACCTTGGG ACACAGTGGG TTAGCCTGGA GAAATGAGA GGCCCTGCCT GGACCCAGGG	1140
	AGAGGAGCCA GTGACACAGG CAGAGCGGTG CAGCCCTCCT TCCCTTCCAT TTGGAGGAGG	1200
	TGGTGCCAGG AGCCTGCCCC CTTACCTCTG CTGAAGCATA AGTGGACTTT GCTTTTGGGG	1260
45	CTTATCTCTG ATACATGCTG GAGCCCTGCC TCTCCACTGC TAGATGGAAC CTGGAATCTC	1320
	TCATCTACCT CTTAGTCTGT CAGTTTCTAC GTGTGAGAAG CAAGCTTGTG GGCCAGTGTG	1380
50	CTGTACATG CTGTAGCACT TAAAAAATAA TTCCAGGGTT CCCTGGAAAA CCAGTCCCAG	1440
	GGTTCCTATG ATCTGTAGTT TCTACCTGGA TTATAACTGG TTTTGGGTAC CTGAATTTTG	1500
	ATTGGTTAGC CTTAATTATA GTCTGGCGTG ATCATGTAGA ATCTTTCTG GTGAACAGAT	1560
55	CATAAGTTC TATCAAGGAG TTCTATCAAG GCATCCATGT CAGTGGTGCT ATGCTGGTTA	1620
	CAACTTGAGA TTTTGAAAT AAAAAATTTG TCATAAAAAA AAAAAAAA	1669

(2) INFORMATION FOR SEQ ID NO: 134:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CACTTTTGCT ATATAACCTA AGTGATAACC CTCTTTTAGT TACCTGCCAA ACTCTGGNCT 60
15 TGGTTTATAT TGCAGTTAAC ACAGTTACAA AGCTGTAATG GTGTCTTTTT TTCCTTTGTA 120
ACCGAATGTG TAAATCAAAG TATATACATT GTGTGGTGT CTGTCTTCTG GAGTTTCATG 180
AGGATTTACA CATGGCATT CAGTGTCTGT ATAGATCTGC CTACCTTTGT GAATTCATCT 240
20 GTTAACCCCT CTCCTTTGA GAGAGCACCG GCGATGGTGG TTAACCTCTT GTGTTTCTC 300
TCTCTCTAC TGGTTATTCT TGAATTAAGC ACAGACTCGT CAGCTCGGTT GCTTTATCAT 360
25 GAATAATGTG TGTGACCTTG CAGTCTTCC ACAGTTCAGC AAACAAGTGC TAGCTTCACT 420
GACCAAAAAT TAAGGAAGGA AAACACAGTT TTTAAAACGA TCCATCTTTT AACAGCCGAA 480
ACCGATGTGT CTATGGTGCT GCACCTTGCT GTTGTACTTC TGAAATCAGA CGTGTGTGAA 540
30 CGATCATTTT TGACTTAACC GTGAGATGCT CACGAGTACC CTCCTGTTG TTTTGTTAGC 600
ATTGAAATCG AGACTATTTA TTTGGAATAT ATACAACAGT GTTTTCCAC TGTATTTTCA 660
35 TTGCAAAAGT TGAGAACTGC TTTCTCTACC TTTTGCAAAA TAATTGATAT TCCATATTGG 720
ATTCTCAAAG ACTTCGATAT GGTGAACCTA TTAACCTAG AAATTGTATT CATCCTTTCA 780
TGACTGTGGC CTGAGTTCCC CAGCCCTCTT CCTCTTTTTT TTTAGATGAG ATTTAGCACA 840
40 CTCTCAGTTA TTTAAACATG CAACATTTCT TGAGTATGTA TGTGAGGCC ATCTGAGCTC 900
ATAGCTGATT CAGTAACCAG TTTTATGCTG TGTCAATCAC ACTCACTACT TAATACTGCC 960
45 ATGGTGAAAA TGTGGAGGAA AAATGTATCC ATGTGTGTCT GGGAAGCATA TACACTTGTA 1020
CATTTTITAA TACTCTGATT CTGTAACATT TCTGAGTTT GTTTTGTTTT ACAGNAAAAA 1080
AAAAAAAAGT GATAAAGCAA TCAGAAGACC AAGAGGTTTA CTATTGATGC TTAGGGTCGT 1140
50 CTGACCTTGG CTGGCCAATA GACCTACACG GCCAAATTAA TTTACGAGAG TAATAATTTT 1200
TCAAAGCCA ATTTTPTTTC TGTATTTTCT GTATGAACT GCCAATATCA TGAATAGAAA 1260
55 GGGAGAACCA TAAAGGAGAA AGAACGTGAT GTTCTGTTAT GTTCATGTAA ACCTAAAGAA 1320
ACAGTGTGGA GGCAGGCGCG ATCAGCCGAA CTCTAGGGAC TTGGTGTGTC TTGGAAGGCA 1380
TCCATACCTG CATTTTGCAT TCTTCGTATG TAATCATATT GCCAAAGACA AACTATTTCA 1440
60

	TCATTTATTG TAAATAACAC TTTTCCCCAG ACCTACCATA AAGTTTCTGT GATGTATTGT	1500
	CTTCCAGTTG CAATAAAAT TACTGAGTTG CATCAATTGA AGAAAAAAAA AAAAAAAAAA	1560
5	CTCGA	1565
10	(2) INFORMATION FOR SEQ ID NO: 135:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2007 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:	
20	TCTAAAAGCC CCCTTATACC CCACTTTGTG CAGCAAAGAT CCCCCTGCAG GTCACAGCCT	60
	GATTGTGGC CAGGCTGGAC AAATTCCTGA GGCACAACCT GGCTTCAGTT CAGATTTCAA	120
25	GCTGTGTTGG TGTGGGACC AGCAGAAGGC AAACGTCCAG CCAACACACA GGA CTGTAAG	180
	AGGACTCTGA GCTACGTGCC CTGTGAAGAC CCCCAGGCTT TGT CATAGGA GGTCGTT CAG	240
	CTTCCCCAAA GTCAGAGGTG ATTTGATTTG GGAAGACTG AATATTCACA CCTAAGTCGT	300
30	GAGCATATCC TGAGTTTAC TTCCTTATGG CTTGCCCTCC AAGTCTCTC TCTCATACAC	360
	ACACACACCC TTGCTCCAGA ATCACCAGAC ACCTCCATGG CTCCAGCTAT GGAACAGCT	420
35	GCATTGGGGC TGCCCTTCTG TTTGGCTTAG GAACTTCTGT GCTTCTTGTG GCTCCACTCG	480
	CGAGGCAGCT CGAGGTGTG GACTCCGATT GGGCTGCAGG CAGCTCTGGG ACGGCACAGG	540
	GCGGGCGCTC TGATCAGCTC GTGTAAAACA CACCGTCTTC TTGGCCTCCT GGCAGTTCTT	600
40	TCTGCGAATA GTCTCTCCC TGGCCAGTTG AATGGGGGAA GCTGCTGGCA CAGGAAGGAG	660
	AGGCGATCCC GGCTGAGGCT TAGGAAATTG CTGGAGCCGG CTCCAAGCAG ATAATTCACT	720
45	GGGAGGTTT TCAGAGTCAA ACATCATTCT GCCTGTCTTG GGGCCAGGT GTGTCACACA	780
	AGCATCTCAA AGTCAAAAGC CATCTGGGGC TGCTGCTTCT CTCTCTCAGG CTCTGGGGAA	840
	AGGAATCTCC CTCTCTCTC ACTTGATTCC AAGTGTGGTT GAATTGTCTG GAGCACTGGG	900
50	ACTTTTPTC TCTTTTCTT GATGGACCAA CAGTGCAAAT GCAATCTCGC CATTTAACTT	960
	TCAGGTGAT TTCTTTCTT GATCAGACAT CTTTGTGCCC CTTTAGGAA GAAAAGAAT	1020
55	ACACCTACGA TGTGCCAGGC ACTGTGTTAG GCGCTTTTAT ATAGATCTC GTTAGGATGA	1080
	GACTAAGGGA TGAGGACATC TCTTTATAAA AGGCCCTAA GTAATGGATA AACAGAAACA	1140
	CTTAGAGGTG AGAAGGTCTG TCTCAAGAT CCAAGGTAAG ATGCTTCA GTCTGATGTT	1200
60	TGTTCTCAAG GACTTATCCC CTACAATATT CTCCACTCC ATACTCTCC TTCTACCCCA	1260

	CCATGTGCTC CCGTGCACTC CTCAGATGGT CAGAGGGGT A ACCCAAGTCC TTAGAGAATT	1320
5	TGGGGACCAA TAGAATATGT GATGTGTGAA TTTTCTTTAA AAAACTTAAG GAGTCTTTGC	1380
	TACCTTCTGC TTGTTGAGTT GTTTTGGCAT TCATATTAAA AGCCAGCATC TCACTATTTA	1440
	TTGACAGGTT GGGCTGTGTG TGTCCGCATG TGTGTATACA TTTCCAGGCG TGCCTGTGTC	1500
10	CTGTAGCTTT TTAAGAGGAA ACCCAGTCAT CCCACTATGA ATCTGGCATC TTCTTATGCT	1560
	TCTAGTGTTC TGGCCATACA TCAACCAAGG GGTTTAATTT ATCCAATGCT TGACGACATG	1620
15	TTCAGGAGGG GCTGGATCAA ATTTTGAGAG GGTATGGA AAGGGAGGG GAGAAGAAAT	1680
	TGACATTTAT TTTATTTATTT ATTTTAAATG TTTACATCTT CTTTATGTTG TATCAAGCCT	1740
	GAATAGAAAC TGATAGCATT AAAATACTCC GTTCTCTCT CTCTTCTCGC TTCCTTTTTT	1800
20	TTTTTTTTTA AATTTAGGAT AACACATTTT TGTTCCTAAA GTGATTTGTG ATTTGTGCTG	1860
	TATAAACTGT ATAAAAGGTT CTGTTTTTAA AGGTGGATTT TCATTCCTCT GGGGACAGTG	1920
25	GTGCGCAAGA CATCTACATT GTAAGAGAAC ACAGTGAAG ATCCTGTCTT GATTCTCAAA	1980
	AATTATTTTC TCTGTATGAT TAAAAGT	2007

30

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

40

	CTTTAACC TCCCCCTCA CACACATACA TATCAGGTG TTTTCTAGTT AAAAACC	60
	GTAGCTCAGA TTCTACTTTA ATGTCAGTGC AGATTGTCAT TGAATCATGC CATTATGTTT	120
45	TTTCTCATTT TTATGCTGTT GGGTCTTAGT TTTTAAATTG ATATAAGAA CTCAGCAATG	180
	GTTTTATTTT CTACTCATAC TTAGGGTTTA GGAAACACTA CCACTAGTTA TCATTTAATC	240
50	AACTTCAATG GTCTACTGAA ACAAAAATGG TAACCTTTTCA TTAGTGGATT ATTTAGAGTT	300
	ATAGTAGTTG TTTCCAGAAA ACACTTCCTC ACAATGTAC TTCCCAATCA AATCATGTGA	360
	TCATACAGTT ATTCCCATGA AAGGCAGAA TTTTGTTC AATTAATCT AGTTTCTGT	420
55	ACATTTAAAT TTGAGAAGGT GACAACTGGC TCTTTCCAG TCTTCCTTCA TGTCAGTTTT	480
	CTGATAGACC ACTATTGGCA AACAGTATCT GTCAACTACC AAATGTGTAA AATTTTCTGT	540
60	ATTTCACTTT GTCTTATTTG TAAATAGTGA ACTAAAAC TTGGCAGATC AGCAACATTT	600

GCTGAGCCTG TTTTMTAAGC TAATGTGTAT TCTTACTAAT GTTCCTATCA AGAATGGATT 660
 TGTAATATAT GCTGTCTATT TCTAATGTTC ACATTCATAT TTTGAGGTTC TATCTTATTT 720
 5 TAATAGAGAA CAGACTTCTC AAAAAATCTT CAGAAGCAGC TTATTATTGA AATATCGAAA 780
 TATTGAAATA AACCCGGTGG GTTAGATTAC TCATCTGTCC ACCAAGTGGG ACATTTGCAT 840
 GGACTGGGGG CTTAAAGGAC TTAGAAGAGA CCTGTAAGTA AATCCTGAAA ATGAGCCAAT 900
 10 CCCCACTTGA ATGGTTACTG GAGTAAACCC ACCTTTACCA CCCCAATTAC AGCACCCGAG 960
 GCCGATAAAC CAACTTGGCT CTGGTTCATT TTTCTTTTCT TCATTTGTGA TGCTCAGATT 1020
 15 CAAAATGTGT GTTCTACACT GTTACAGGCT TCTCTTTTGT TTGATTAAAG ATTTTAGTCC 1080
 TACTTTTGTA TGGACACATT AGAATATTCA GAGACCAAAA TAGAAGAATT TGCTGTTAGA 1140
 TATTTTTCAG AAGTCAGCAG ATTTGTGGCA AATCATTTAT TTGCCTTTTT AAAAATTCAT 1200
 20 TTAAGCAGTT CAGAGAGTAG ACTACTCAGA AAATTATTTT ACGTAATTGT CTAAGAGGTC 1260
 AATATTTTTT AATGCATATT GAATCAAATA A 1291
 25

(2) INFORMATION FOR SEQ ID NO: 137:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1906 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GGCACGAGGA CCTACTTTTG TAACAGACCA TGGTGTGTGTC CAAGGTAAAA CCACAGTGAT 60
 40 ATTTTGGGAT GCTTTGTCTG CAATCTTGAC TTGTTTTTGC AGTATCATTA TTCAGACTTC 120
 AAATTGTGAA TCTTTTAAAC ATCTTGATAA TTTGTTGTG AGAGCTGTTC ATTCTAAAAT 180
 GTAATGAAAT TCAGTCTAGT TCTGCTGATA AAGATCATCA GTTTTGAAAG GTTACTGATT 240
 45 TTCTCTTCC CTCTTAGTTT TTTACCCAAT ATATGGAGAA GAGTAATGGT CAATCTTAAC 300
 ATTTTGTMTT AATTGTTTAA TAAAGCTGCT GGCAGTGGT GCAGCAITCC TACCTAGTGT 360
 50 CATAAAAGCA AAATACCTAC ATAGCTTTCT TAAATATAG GAATGACATT ACATTTTITAG 420
 GAGAAAGTAA GTTGCTTTGC ACCGCCTACT TAATTCCTTT CCATATATTG TGATACAAAC 480
 TTTTGAATAT GGAATCTTAC TATTTGAATA GAAATGTGTA TGTATAATAT ACATACATAC 540
 55 ATAAGCATAT ATGTGTGTGT GTGTGTGTAT ATATATATAT ATGCATGCTG TGAAACTTGA 600
 CTACACAACA TAAATCACTT TTTAAATTCC AGGAACGGGT AGTCTGACAC GGTGATTATC 660
 60 CTTTGTAGGC TGAATCCGTT ATTAACCTGT TATTTAGGTT TTACTCCAG TAGCAAGGGA 720

	TTCTAAGTTA GTTGCACTTA CATGATTATT GTGATTTAAA ACTAAGAATA AAGGCTGCAT	780
5	TTTCAAAGAT AAATTGGAAT TGCTGTTGGT GAAATAACAA CCAAATACT GAATCTGATG	840
	TACATACAGG TTTCTACAGG AAGAGATGGT ATAATTTACA ATTTGGAGAT TTAATAACCA	900
	GGGCTACCCA GAAAAAGTGA CTTGATAACA TGGTACCAAT AAGTAAGGA TGCTCTCTCG	960
10	GMTTGCTTTT GCCACTTTCA AGATTTTAACT TTCTCAGGTT ATTAATCAAA ATTATGTAT	1020
	AAGTTAGCCA ATAGAATTTT TAGGTTAAAA CAACAGATGG GGGGTTTGTG GAGTGTTTAA	1080
15	TGTCATGGGC ATTTTTAGTA GCATAGACCC TTGTTCTGTC ATTTGAATGT TTCGTATATT	1140
	TTTGTTTCAC AGTTAATCTT CCTCCCCAA GTTTGCTATT CAAATCAACT GCCTGAATGA	1200
	CATTTCTAGT AGTCTGATGT ATTTTCTGA GGAATAGTTT GTGATTCCAA TGCAGGTGTC	1260
20	TTCAATTACCA TTACCTCTAC ACTGCAGAAG AAGCAAACT CCTTTATTAG AATTACTGCA	1320
	CATGTGTATG GGGAAAATAG TTCTGAAAGG CTAGAATGAT ACAAGTGAGC AAAAGTTGGT	1380
25	CAGCTTGGCT ATGGAGTGGT GGCAATAATC TCTAAACATT CCAAAGACC ATGAGCTGAA	1440
	CCTAAACTCC CTGCGGAATC TGAACAAAG GAATATGAAA ATTGCCATTT GAAAACTGAC	1500
	CAGCTAATCT GGACCTCAGA GATAGATCAG CCAGTGGCCC AAAGCCATTT CAAGTACAGA	1560
30	AATATAGAG ACTACAGCTA AATAAATTG AACATTAAAT ATAATTTTAC CACTTTTGT	1620
	CTTTATAAGC ATATTTGTAA ACTCAGAACT GAGCAGAAGT GACTTTACTT TCTCAAGTTT	1680
35	GATACTGAST TGACTGTTCC CTATCCCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA	1740
	GTGCACAACT TAGGTTATTT TTGCTTCCGA ATTTGAATGA AAAACTTAAT GCCATGGATT	1800
	TTTTTCTTTT GCAAGACACC TGTTTATCAT CTGTTTAAA TGTAATGTC CCCTTATGCT	1860
40	TTTGAAATAA ATTTCTTTT GTAAAAAAA AAAAAAAAAA AAAAAA	1906

45 (2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1935 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

55	TCTGAATAA TGCTAACAGA TCCCCCTGAG GGATTCTTGA TGGGCTGAGC AGCTGGCTGG	60
	AGCTAGTACT GACTGACATT CATGTGATG AGGCAGCTT TCTGGTACAG GATTCTAAGC	120
60	TCTATGTTTT ATATACATTT TCATCTGTAC TTGCACCTCA CTTTACACAA GAGGAACTA	180

	TGCAAAGTTA GCTGGATCGC TCAAGGTCAC TTAGGTAAGT TGGCAAGTCC ATGCTTCCCA	240
	CTCAGCTCCT CAGGTCAGCA AGTCTACTTC TCTGCCTATT TTGTATACTC TCTTTAATAT	300
5	GTGCCTAGCT TTGGAAAGTC TAGAATGGGT CCCTGGTGCY TTTTACTTTT GAAGAAATCA	360
	GTTTCTGCCT CTTTTTGAA AAGAAAACAA AGTGCAATTG TTTTITACTG GAAAGTTACC	420
10	CAATAGCATG AGGTGAACAG GACGTAGTTN AGGCCTTCCT GTAAACAGAA AATCATATCA	480
	AAACACTATC TTCCCATCTG TTTCTCAATG CCTGCTACTT CTGTAGATA TTTCATTTCA	540
	GGAGAGCAGC AGTTAAACCC GTGGATTTTG TAGTTAGGAA CCTGGGKTCA AACCCCTCTC	600
15	CACAAATTGG CTATGTCTCT GGACAAGTTT TTTTITTTTT TTTTITTTAA ACCCTTTCTG	660
	AACTTTCACT TTCTATGTCT ACCTCAAAGA ATTGTTGTGA GGCTTGAGAT AATGCATTTG	720
20	TAAAGGTCT GCCAGATAGG AAGATGCTAG TTATGGATTT ACAAGGTTGT TAAGGCTGTA	780
	AGAGTCTAAA ACCTACAGTG AATCACAATG CATTTACCCC CACTGACTTG GACATAAGTG	840
	AAAAC TAGCC AGAAGTCTCT TTTTCAAATT ACTTACAGT TATTCAATAT AAAATTTTGT	900
25	TAATGGATAA TCTTATTTAT CTAAACTAAA GCTTCTGTT TATACACACT CCTGTTATTC	960
	TGGGATAAGA TAAATGACCA CAGTACCTTA ATTTCTAGGT GGGTGCTGT GATGGTTCAT	1020
30	TGTAGGTAAG GACATTTTCT YTTTTTCAGC AGCTGTGTAG GTCCAGAGCC TCTGGGAGAG	1080
	GAGGGGGTA GCATGCACCC AGCAGGGGAC TGAAGTGGG AACTCAAGGT TCTTTTACT	1140
	GTGGGGTAGT GAGCTGCCTT TCTGTGATCG GTTCCCTAG GGATGTTGCT GTTCCCTCC	1200
35	TTGCTATTCT CAGCTACATA CAACGTGGCC AACCCAGTA GGCTGATCCT ATATATGATC	1260
	AGTGCTGGTG CTGACTCTCA ATAGCCCCAC CCAAGCTGGC TATAGGTTTA CAGATACATT	1320
40	AATTAGGCAA CCTAAAATAT TGATGCTGGT GTTGGTGTGA CATAATGCTA TGGCCAGAAC	1380
	TGAAACTTAG AGTTATAATT CATGTATTAG GGTCTCCAG AGGGACAGAA TTAGTAGGAT	1440
	ATATGTATAT ATGAAAGGA GGTATTAGG GAGAACTGGC TCCACAGTT AGAAGCGAA	1500
45	GTGACACAAT AGGCCGTCTG CAAGCTGGGT TAGAGAGAAG CCAGTAGTGG CTCAGCCTGA	1560
	GTTCAAAAAC CTCAAAACCTG GGAAGCTGA CAGTGCAGCC AGCCTTCAGT CTGTGGCCAA	1620
50	AGGCCAAGAG CCCCTGGCAA CCAACCCACT GTTGCAAGTC CTAGATTCCA AAGGCTGAAG	1680
	AACCTGGAGT CTGATGTCCA AGAGCAGGAA GAGTGAAGA AAGCCAGAAG ACTCAGCAAA	1740
	CAAGGTAGAC AGTGCTTACC ACCAYAGTGG CCATACCAA GAGGCTACCG ATTCCTTCCT	1800
55	GCTACCTGGA TCCCTGAAGT TGCCCTGGTC TCTGCACCTT CTAAACCTAG TTCTTAAGAG	1860
	CTTTCATTA CATGAGCTGT CTCAAAGCCC TCCAATWAAT TCTCAGTGTA AGYTTCAAAA	1920
60	AAAAAAAAA AAAAA	1935

(2) INFORMATION FOR SEQ ID NO: 139:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

15	NGCCCCCTTG GCACAAGTCA GATGAAGCAC GTTCTGCCGG GGAGGCCCTC AMCTTCCAGA	60
	GAGGACAGAC ACAGATTTCC TGCTGGGGGA GGGAGGAGTC CACGCATCCT GATGCTGCCT	120
	GGAAGCTTAT TTTCCCGTGG CCAGGATGCA TTTCTCTGAG TGGAAACAGG TTCTTGCA TG	180
20	TGGATGTGTG TTTCCCCAGG CAGACGGCCC CTCTYTTCCC AGCACTTCCC TGCCTCCCCC	240
	AGGCCTCAGG CCAGCACCCA GTTCTCTCCTC ACATGGCAGG TGAGCACAGA CTTCTAGTTG	300
	GCAGGAGCTG AGGAGGGTGA ACAAACCCCG AGGGAGGCCG GGCCCTTGCT CCCGAGTTGG	360
25	GGGGAGGGGG TGTGGCAACG TGCCCCCGC AGAGGCCACG CATGTTTGAC CAAAGCCCTC	420
	ATTGTGGTCC GAGGACAGCC TTTTCCCCAG GCCTCARAGC ATTGCTCATC CGTGCCAAAC	480
30	TGGGTAGGTG GATTTGAGCG GAAAGACTCC CAAATGTGC CAAGAATTTC CCRGTCCCAG	540
	GCAGGGCAGG GGAAACTAAG GGCAAGCAGG ATACAGGGCG AGGGATGTGG CAGGTGAGGG	600
	GGCTCCCGCC TGTGCCCTTT CTCTCACCA TGTCTCCCCC ACCCTGCCTC AGTTCTCCGT	660
35	TCCCCCTCAT CTCCGTCCCC CTCTTTGAAG CTGTCCCCAT CTCAGTGTCA GACCAGCCTT	720
	CTCTCAKCT GACCACCTC CTCTGACCSA CGCCCCCTCC TTGTCTGAAA AAAGGAGCCT	780
40	TGAATGGTGG AGGGAGGCAG TGGGGAGAAA GGTCTCACCG GACAGGTTGG GAGAATGAGG	840
	TCAGCGGTGC TGGGGAACAG ATGGAGGGGG CAGTGGGGAC AGGGCTTGGG CAGACACCAG	900
	CAGGAATAAT TTGAAATGTG TGAGGTGACT CCCCGGAGGC CTTGGGCTTG GGCATTTGGG	960
45	AAAAGAATGA TGTCTGGAAG GGCTTAAGGG ACACAGTGA CGAGGGGAGA GTCCTCATCT	1020
	GCTGGCATTT TGTGGGTGT TAGTGCCAAA CTTGAATAGG GGCTGGGTG CTGTCTTCCA	1080
50	CTGACACCCA AATCCAGAAT CCCTGGTCTT GAGTCCCCAG AACTTTGCCT CTTGACTGTC	1140
	CCTTCTCTTC CTACCTCCAT CCATGGAAAA TTAGTTATTT TCTGATCCTT TCCCCTGCCT	1200
	GGTCTAGCTC CTCTCCAAAC AGCCATGCCC TCCAAATGCT AGAGACCTGG GCCCTGAACC	1260
55	CTGTAGACAG ATGCCCTCAG AATTGGGGCA TGGGAGGGGG GSTGGGGGAC CCCATGATTC	1320
	AGCCACGGAC TCCAATGCCC AGCTCCTCTC CCAAAACAA TCCCACAAAT CCCTTATCCC	1380
60	TACCCCAACC CTTTGGGGCT CTGTACACAT TTTTAAACCT GGCAAAAGAT GAAGAGAATA	1440

TTGTAA

1446

5

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1109 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TTTTTTTTTT TTTGATATGA AATTGTCTTT CTCCATTGCA GAAATAAGCT AGGGAAACAC 60
TAACCCAAAA ACTTCTGTGA GAGCTGTTC TTTGGAGGCA GCATCACTTA TTGGCAGTAA 120
AGACTCAGTA TAAAAGCACC AGCATCCCTA CTGGGGTGAT GGGGATTAAT TTTATAGCAT 180
TCCATTTTCC TAGTGCCACA TGTGAAATTG GATTTTGATG ATCTTAATCT ATATTCTACC 240
CTTATAATAA AAGATCAAAA GATATATCTC CTATGAACAG ATTGGAGATA GGAGATGAAA 300
AGTTGGGAGG ATGTCTTTAT TCTAATGTGA GGGTAGGGAA AATGTGGATA ACATTACTGG 360
GGTGARGGAG GCATGTGTTCT TTAGTTGGAG TTCTCATTTT TATTCTCCAG TACTGACTTG 420
TGGGGAAAGC ATACTTTTTC ACTGCCAGGT ACTGAATGCA GAGGCTCAGT GAAGTATATA 480
TGTGGGAAGT GCATGCATTT CGTTTATTAG CAAACATAGC TGGATTAAGA CAAAGTTGTT 540
GGTTTGAAAA GGGGTAAAG CCTTAAGTGA ACAAATCTAG CTAACAGTGA ATGAACTAGG 600
TAATATAACT TGCATATTTT TAATTTCCCT TGGTTAAAGG TCCCCCATACTTCTCTGTTT 660
GGAGACATGA GAAGTATGAT TACTTCAGTG TTAGTTTCTT TAATTTTTTT TTCCCTAT 720
TTGTCCCTTG TCACTTTGTT GCAAGCTAGA AATCTGTGGG TTATACATAG GGCAGCTCTT 780
TGTGAAAGTG GTTTATTCCA CTGGAGAAAG GGGATTGAAA ATCAGTTAGA ACCAATGTAT 840
TTCTTGCCCC ACGGAACACT ATTCTATATA GATAGCTGAA AGAAGCTGCT GTGAGGAGCT 900
CAGCTCCAAA CACAGGATCA GCACCTTGTA TAGGAATTCC CATGAATTAT GACTTCTCAT 960
TCTGTTTTAT CAGAGTGCAT ATATGTCCTA CTTGAGGAAA AGTAAAACAG TCATTACGA 1020
AAGAAAGTCA ATCTGTATCC TAAGCATTTT AATAAAAAGT TAAAACAAA AATTAAAAGG 1080
GACACTCGAG GGGGGGCCCC AAACCCAAT 1109

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(2) INFORMATION FOR SEQ ID NO: 141:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TAGGACTAAC TTAAATTCCT TTATTCATCT TTTATTTATT AAAAAATTTT ATTTCCTTGA 60
 10 ATTTTCCTGT AATTTCCTTA RGCTCTTCTA TAAAATGTTA TATTCATGTG AACCATACCT 120
 CATTATCCCT AACATTTACT CTCAAAAAGC TTTTATTTTT TATTTTTTTG AAGGTAGTTT 180
 TTCTGTGTGT ACTCTGTAAC ATGATTTTGC TTTCAAATCA TTGTTGTGCC CCCATACAAA 240
 15 ATGCCCTTTTA TTTTGTAGGA TCGTGGACTT TTTAGTATGG CATGAGTGTG CTAAAAGCCA 300
 GATATCTTTC CACATTCACT GGTGGCTTTG ACACCTAGTT TTTAATCTCC CATCCTTACT 360
 20 TTAAACCCTG ACAGTGCAGT CCTCAGTCAG GGCCAGGACC GGGCTGAGGC CCTTTGTGGA 420
 GATGCTGCAC CACCAGCAGA AGGCTGAGAC CTGGTTACCT GTACCTGTTT ACTTGTAATA 480
 AAAAGAATTA TCTAAAA 497
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(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATGAGGCAGA GGCAAGCTGC CTGCCAACCC CCTCCCTCAA GGAATGGCCT TGCCAGGAA 60
 40 TGCCACCAC ACATACCTC TTCTTTTTT CTAGTCAAAC TCTGTATTAT TCCTGGCTT 120
 GCCTCCCTCC TTTCCTCCCC TCTCAACCTT TTAATTCTGG TTTCTATTTC ATGGGATTTG 180
 45 GGGTTGAAGT TAAACTTACA ACAGTGCCGC CAACACCAAG TCTTGCAGGA AAAAAATACA 240
 AAGAAATTTA ACAAAAAAAA AAAAAAAA 269

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(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

TTGATTGACT ATGGTCTCTC CGGCTACCAG GAAGAGTCTG CCGAAGTGAA GGCCATGGAC 60
 TTCATCACCT CCACAGCCAT CCTGCCCTG CTGTTCCGGT GCCTGGGCGT CTTGGGCTC 120
 5 TTCCGGCTGC TGCAGTGGGT GCGCGGGAAG GCCTACCTGC GGAATGCTGT GGTGGTGATC 180
 ACAGGCGCCA CCTCAGGGCT GGGCAAAGAA TGTGCAAAAG TCTTCTATGC TCGGGTGCT 240
 10 AAATGGTGTC TCTGTGGCCG GAATGGTGGG GCCCTAGAAG AGCTCATCAG AGAACTCACC 300
 GCTTCTCATG CCACCAAGGT GCAGACACAC AAGCCTTACT TGGTGACCTT CGACCTCACA 360
 GACTCTGGGG CCATAGTTGC AGCAGCAGCT GAGATCCTGC AGTGCTTTGG CTATGTGAC 420
 15 ATACTTGTCA ACAATGCTGG GATCAGCTAC CGTGGTACCA TCATGGACAC CACAGTGGAT 480
 GTGGACAAGA GGGTCATGGA GACAACTAC TTTGGCCCG TGTCTTAAC GAAAGCACTC 540
 20 CTGCCCTCCA TGATCAAGAG GAGGCAAGGC CACATTGTGC CCATCAGCAG CATCCAGGGC 600
 AAGATGAGCA TTCCTTTTCG ATCAGCATAT GCAGCCTCCA AGCACGCAAC CCAGGCTTTC 660
 TTTGACTGTC TGCCTGCCGA GATGGAACAG TATGAAATTG AGGTGACCGT CATCAGCCCC 720
 25 GGCTACATCC ACACCAACCT CTCTGTAAAT GCCATCACCG CGGATGGATC TAGGTATGGA 780
 GTTATGGACA CCACCACAGC CCAGGGCCGA AGCCCTGTGG AGGTGGCCCA GGATGTTCTT 840
 30 GCTGCTGTGG GGAAGAAGAA GAAAGATGTG ATCCTGGCTG ACTTACTGCC TTCCTTGGCT 900
 GTTTATCTTC GAATCTTGGC TCCTGGGCTC TTCTTCAGCC TCATGCCTCC AGGGCCAGAA 960
 AAGAGCGGAA ATCCAAGAAC TCCTAGTACT CTGACCAGCC AGGGCCAGGG CAGAGAAGCA 1020
 35 GCACTCTTAG GCTTGTCTAC TCTACAAGGG ACAGTTGCAT TTGTTGAGAC TTTAATGGAG 1080
 ATTTGTCTCA CAAGTGGGAA AGACTGAAGA AACACATCTC GTGCAGATCT GCTGGCAGAG 1140
 40 GACAATCAAA AACGACAACA AGCTTCTTCC CAGGGTGAGG GGAAACACTT AAGGAATAAA 1200
 TATGGAGCTG GGGTTTAACA CTAAAACTA GAAATAACA TCTCAAACAG TAAAAAATAA 1260
 45 AAAAAAAC 1269

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1944 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

AAAAGGCAAA CTATAGGATA ACACAGAGCC CTTTTTGAAA ATAAATTGGC ATTGGAGTGT 60

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	TTTACCCTCT AGCTGTTTTA CTTAGAATGT AACATATGCT GCCTACCCAC CTCAAAATGT	120
	CTGTACTGCA AGAGGGCCCT GGGCCTCTGC TTTCCATATT CACGTTTGGC CAGAGTTGTA	180
5	GTCCCAAAGA AGAGCATGGG TGGCAGATGG TAGGGAATTG AACTGGCCTG TGCAATGGGC	240
	ATGGAGCACA AGGGGTCACA GCATGCCCTCC TGCCTTACCG TGGCAGTACG GAGACAGTCC	300
10	AGAACATGGT CTTCCTTGCCA CGGGGTGTTG TTGTCTCTGG TGGTGCTGCA TGTCTGTGGC	360
	TCACCTTTAT TCTTGAACT GAGGTTTACC TGGATCTGGC TACTGAGGCT AGAGCCCACA	420
	GCAGAATGGG GTTGGGGCTG TGGCCCCCAA ACTAGGGGGT GTGGGTTTAT CACAGTGTG	480
15	CCTTTTGTCT CCTAAAGATA GGGATCTACT TTTGAAGGGA ATTGTTCTC CCAAATAAAT	540
	TTGCTTTACC TTGGTCCCTT CTTTTGTGCC AGTATTCAAG TGGTATAGCT CTGAGCAGGG	600
20	TCACATTTGG CCAAACCTGA CACTGTCTTG CTGCATCTC CTTTGGCAA CATCAGGGTC	660
	AGAATTCAGG ATAGCCCTTC CTAGGGCACT GGACTTTCTG GCATGGGGC TGTGTTTGCA	720
	CAAGTTATTT TCATGTTACC TGGAGAGTGT CCAGAGGCTG CTCTGAGGCT GAGGTGTGTT	780
25	CCCCCTTGCC TGGTTCACG GTTCAGAGGG ATACCATCCT AGGGTCTGGG AATCCAAGGC	840
	CACGAGACTC CTTGGTTTGT GGTCCGAGAT CCTGTACTAA GGAGGGTCTG GCCAGAGGAA	900
30	CAGACCAGCT TTTGCACAAT GAAGCGCAAG GGAACAAGTG GTTTGCCTGG TGTCTTACCT	960
	GTCTGAACC TGGTCTGTG GGCCATTGAA AAGTTAGATC TGTGATCTCT GGGGTTTTTG	1020
	TGGCTTTGTT CAATGCTTCC ACTCTAGGGC AGGCAGAGCA GTCTATACTC TCCCAAGCCT	1080
35	GCTTGACCTC CAAGTAGAGC TGATACAGAG ATCTGTGAAT ATTGTGATAG AAATTCTTTG	1140
	GTATTCATAC ATTTACAGCT CAAGTCAGCA ATTTCCAGG TACCATGTAA GCTATAAAAC	1200
40	AGTCATTCTT AAAGACAGAG GATAGCTGTG ACTCATGGGA TCATGAGGTC CATGGCTGGT	1260
	TGCAGGTTCC CTTTTCTCTT CTCAGGTTT TGTCTCTTCC TGTGTTGTCC CCAGCAAGGG	1320
	AGAGACTGTG GGGTGGATTG GGAGAACAGA TTAGGAGTAT AGCAAATGAA CCCAGAATGG	1380
45	AACAGTGGGG AGCTAACTGT GAATGAGGAG AGTACCTGCT GCAGGACCTG GAGGTCAGGT	1440
	GTGAATGCTG TATTGGCACA GGAATAAAT ATCCTGGCGT CTGGAGCCTT CACCTCTCCG	1500
50	TCAAGTCCCTT CCTGTGATAC TGCCATGGCA CAGGATCTGA GTTGCAGCTC TGCACCCTAA	1560
	ATCACACCCT GGGCATTGTC TGGGCTGCAG GGCTGCCAGG TTCTGTACTT GTGTCCAGCT	1620
	GTGGCCCTGG ATGCTGGAGC TGGAGGGTTT TCTGTGCTCA GACTGTAGCC TGTAGCTCTT	1680
55	GGCCTGTGTA GAGCCCCCTC CTGTGCCCTC AGTGGCTGTC GTTTGTTAAC ATCATCAGGA	1740
	AGATGGGAAA GGTCAAGCAG AATTTTTCTG CCCTACAAAG GTTGAAGAG AAAGGACACA	1800
60	GTATTTTCAT GAATTTACCA TATATCTTTG TTTTCTTCA ACGAAAAAGT TAATTGAGGC	1860

AATGTCATCT GCTCAAAGTT GAGTGGTTTA TTCACAATAA ACTGTAAGTT TCTGATTATA 1920

AAAAAAAAAA AAAAAAAAAA AAAG 1944

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(2) INFORMATION FOR SEQ ID NO: 145:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1021 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

TCGACCCACG CGTCCGGGGT GCGCAACGGG GAGTTCCGGC TGGAGACCCG TGCTCTGGGC 60
20 CGGCGCCTTC ACCATGGCCT CGGCAGAGCT GGA CTACACC ATCGAGATCC CGGATCAGCC 120
CTGCTGGAGC CAGAAGAACA GCCCCAGCCC AGGTGGAAG GAGGCAGAAA CTCGGCAGCC 180
TGTGGTGATT CTYTTGGGCT GGGGTGGCTG CAAGGACAAG AACCTTGCCA AGTACAGTGC 240
25 CATCTACCAC AAAAGGGGCT GCATCGTAAT CCGATACACA GCCCCGTGGC ACATGGTCTT 300
CTTCTCCGAG TCACTGGGTA TCCCTTCACT TCGTGTMTTG GCCCAGAAGC TGCTCGAGCT 360
30 GCTCTTTGAT TATGAGATTG AGAAGGAGCC CCTGCTCTTC CATGTCTTCA GCAACGGTGG 420
CGTCATGCTG TACCGCTACG TGCTGGAGCT CCTGCAGACC CGTCGCTTCT GCCGCTGCG 480
TGTGGTGGGC ACCATCTTTG ACAGCGCTCC TGGTGACAGC AACCTGGTAG GGGCTCTGCG 540
35 GGCCCTGGCA GCCATCCTGG AGCGCCGGG CCGCATGCTG CGCCTGTTGC TGCTGGTGGC 600
CTTTGCCCTG GTGGTCGTCC GTTCCACGT CCTGCTTGCT CCCATCACAG CCNTCTTCCA 660
40 CACCCACTTC TATGACAGGC TACAGGACGC GGGCTCTCGC TGGCCCGAGC TCTACCTCTA 720
CTCGAGGGCT GACGAAGTAG TCCTGGCCAG AGACATAGAA CGCATGGTGG AGGCACGCCT 780
GGCACGCCGG GTCTTGGCCG GTTCTGTGGA TTTGTGTCA TCTGCACAG TCAGCCACCT 840
45 CCGTGACTAC CCTACTTACT ACACAAGCCT CTGTGTCGAC TTCATGCGCA ACTGCGTCCG 900
CTGCTGAGGC CATGTCTCCA TCTACCTCT GCTCCAGAAA TAAATGCCTG ACACCTCCCC 960
50 ACAAAAAAAAA AAAAAAAAAA ACTCGAGGGG GGGCCCGTA CCCAATTCGC CCTATAAAG 1020
T 1021

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(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

GGCACGAGGA GGGCCACGGC AGCCATCGCG CTTTGCAGTT CGGTCTCCTG GTGTACGGCC 60
AACGCCAAGT AGGGGATTGC GTTCCCTCCA GTCGCAGACC CTATCAGATT TGGATATGTC 120
10 CTTTCATATTT GATTGGATTT ACAGTGGTTT CAGCAGTGTG CTACAGTTTT TAGGATTATA 180
TAAGAAACT GGTAACTGG TATTTCTTGG ATTGGATAAT GCAGGAAAA CAACATTGCT 240
15 ACACATGCTA AAAGATGACA GACTTGGACA ACATGTCCCA ACATTACATC CCACTTCCGA 300
AGAACTGACC ATTGCTGGCA TGACGTTTAC AACTTTTGAT CTGGGTGGAC ATGTTCAAGC 360
TCGAAGAGTG TGGAAAACT ACCTTCCTGC TATCAATGGC ATGTATTTTC TGGTGGATTG 420
20 TGCAGACCAC GAAAGGCTGT TAGAGTCAAA AGAAGAACTT GATTCATAA TGACAGATGA 480
AACCATTGCT AATGTGCCTA TACTGATTCT TGGGAATAAG ATCGACAGAC CTGAAGCCAT 540
25 CAGTGAAGAG AGGTTCGAG AGATGTTTGG TTTATATGGT CAGACAACAG GAAAGGGGAG 600
TATATCTCTG AAAGAACTGA ATGCCCGACC CTTAGAAGTT TTCATGTGTA GTGTGCTCAA 660
AAGACAAGGT TACGGAGAAG GCTTCCGCTG GATGGCACAG TACATTGATT AACACAACT 720
30 CACATTGGTT CCAGGTCTCA ACGTTCAGGC TTACTCAGAG ATTTGATTGC TCAACATGCA 780
TAACTTGAAT TCAATAGACT TTTGCTGGTT ATAAACAGA TGTTTTTTAG ATTATTAATA 840
35 TTAAATCAAC TTAATTTGAA TGAGAATTGA AAACGTATTC AAGTAAGTTT GAGTATCACA 900
ATGTTAGCTT TCTAATTCCA TAAAAGTACT TGGTTTTTAC AGTTTATAAT CTGACATCAC 960
CCCAGCGCCA TTTGTAAAGA GCAACTTTCC AGCAGTACAT TTGAAGCACT TTTTAACAAC 1020
40 ATGAAACTAT AAACCATATT TAAAAGCTCA TCATGTTAAA TTTTTTATGT ACTTTTCTGG 1080
AACTAGTTTT TAAATTTTAG ATTATATGTC CACCTATCKT AAGGTACAG TTAATAATTA 1140
45 GCTTATTCAA TGATTGCATG ATGCCTTACA GTTTTCAATA ACTTTTTTTC TTATGCAAAC 1200
GTCATGCAAT AAAACAACT CTAATGTTTG GCAAAAAAAA AAAAAAAAAA NTCGAGGGGG 1260
GGCCCGTACC CAATTGCCCC TAAAG 1285
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(2) INFORMATION FOR SEQ ID NO: 147:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5	GGCACGAGGT GGCACGAGGG TCAGTGGTTC TCTCGGTCT CGGCACAGGT GAGCACCTG	60
	ATGAAGGCCA CGGTCCTGAT GCGGCACCTG GCGGGGTGCA GGAGATCGTG GCGCCCTCC	120
	GCAAGGGCGS CGGAGACCGG TTACAGGTGA TTTCTGATTT TRACATGACC TTGAGCAGGT	180
10	TTGCATATAA TGGAAAGCGA TGCCCTTCTT CTTACAATAT TCTGGATAAT AGCAAGATCA	240
	TCAGTGAGGA GTGTGCGAAA GAGCTCACAG CGCTCCTTCA CCACTATTAC CCAATTGAGA	300
	TGACCCACA CCGGACCGTC AAGGAGAAGC TACCTCATAT GGTGGAATGG TGGACCAAAG	360
15	CGCACAATCT CCTATGTCAG CAGAAGATTC AGAAGTTTCA GATAGCCCAG GTGGTTAGAG	420
	AGTCCAATGC AATGCTCAGG GAGGGATATA AGACCTTCTT CAACACACTC TACCATAACA	480
20	ACATTCCCTT TTTTCATCTTT TCTGCGGGCA TTGGTGATAT CCTGGAAGAA ATTATCCGAC	540
	AGATGAAAGT GTTCCACCCC AACATCCACA TCGTGTCTAA CTACATGGAT TTTAATGAAG	600
	ATGGTTTCTT CCAGGGATTT AAGGGCCAGC TGATACACAC ATACAACAAG AACAGCTCTG	660
25	TGTGTGAGAA CTSTGGTTAC TTCCAGCAAC TTGAGGGCAA AACCAATGTC ATCCTGCTGG	720
	GAGACTCTAT CGGGACCTC ACCATGGCCG ATGGGGTTCC TGGTGTGAG AACATTCTCA	780
30	AAATGGCTT CCTGAATGAC AAGGTGGAGG AGCGCGGGA NCGCTACATG GACTCCTATG	840
	ACATCGTGCT GGAGAAGGAC GAGACTCTGG ATGTGGTCAA CGGGCTACTG CAGCACATCC	900
	TGTGCCAGGG GGTCCAGCTG GAGATGCAAG GCCCCTGAAG GCGCAGGCTN CCAGNCCGCC	960
35	TGCAGGCCGT GGTGAGGAGG GCGCCTCCC CAGAGTCTGC TCCCCCGTGA ACACAGAGCA	1020
	GANGCCAGGG TGGCCAGCAG TGGCTGGGTC CTTCGCGGCC CCTCCGTCCT CTTTCCCTG	1080
40	AGCACCTTCA TCACCAGAGG CTTGAAGGAA CCCC GCCATG TGGCAGGCA CAGGCACTGT	1140
	TCCTGGTGAA CCTTGGACCA CAGCATGTCA GTGCTCTAGG GATTGTCTAC TCCAGGGATT	1200
	TTCTTCAAAA TTTTAAACA TGGGAAGTTC AAACAAATAT AATGTGTGAA ACAGATCAAA	1260
45	ATTTTAAAAA TGAATAAAAA GCTGCTCTGA TTCAGGGGAT GTGGGTGCGG GTAGAACCTG	1320
	GACCTCTTGG CCTGGGGGCA CATGGGATGC TTCTAGGAAC ACAGTTTGAG AACCACCAAA	1380
50	AAAAAA	1386

55 (2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 2098 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

5	AGCCCTTCTC CCCGCGCTTG GGA CTCTGAC ATCTTAAGGC TGCACGGTCG TGTCTTGTC	60
	TGGGTGAGGC CATGTCTGTG ATCCAAGGTT CCTGGAAC TG ACACAGGAAG GGGCTGTGAA	120
	CCCTAAGTGG GTGTMATCTC CTCCRACCGA GGCTTCTMAC CCTGGAGATG GCAGTTACTC	180
10	CTGGCCATGG TTGCTGAGCA TGGGCAGACC AGTGGAGGCC ACCCTACTGT GTTATCTGCG	240
	CCTTCRATGA AGTGAGACCC TTGGGGAGAA CGGGCTGTGG ATGAAGGAGT GGA CTGCAGC	300
15	CTTGGCCTAG CCACTGGGCT GGGATCTTCT GGGTCATGTG ACTGTGTATC CAGGAGCAGA	360
	AAC TTGTATT CTCAGGATTC AGGATCTACC CAGCACCAA GATGTATTTT CAGGAGAACA	420
	GACCTAGAAA TGGGCCTGTC TGGCATTTC AAGTCAGGCA AAGCAGGCAG GGCCAGGGAG	480
20	CTTCTGTGGG TCTACACAAG AAGGTTCTCTG TGAGGGCTAT CAGTTGTGTC CTCTAGCTT	540
	GCTGGTAACT TTGGCGCCTC CGCCAAGCCC TGCCAGACTC CCCTGGCTGT GATGGCATTC	600
25	TGTGCCATCC TGCCTTGTC CCAGCCTCTG CAGGATGCCC TCCCTACCCA MCTYTYCCTG	660
	GGCCTTCCCT GTCCACTGGG CTGGATT CAT GTTCAAACCA CTGGACTGGC AGGGCAACGA	720
	CTTCTTCCCA CCTCAAGATG AGGTCTCTGC CCCCTTGTCT TGGCATAAAA ACACCTTTAA	780
30	AGCATGAGCC ATGTGCTTCT TTGCCCTTCT CTGTCTGTGT CCAATCTTCT GCCTCCAGT	840
	CACTCCCTGG GGA CTATGGG ATCACTGTCC CCCCACCTGT GTGGCCACAC CATGTGTCTT	900
35	GTCAATCCAG AACTGCCTCT GAGCTCCAGG CTGACCACAG ATCAGCCACA GCCTGATGCC	960
	TGCAGCCCCA CTTTGCTCAC CTTTCCCTC CCCTCCTCCT TCCTTCCACA CAGCAAGCCT	1020
	ACCTTTFYTC ATCCATGCTC ACCATAGCCC CCTTCCTTGT GACCTGGACC CTCCATTGTA	1080
40	CCTGGCTGAG ACTGTGAGCC TCCTGGAGGA GTGGGGTCCA CCTTCTTCTT GCCCTATGCA	1140
	GTGCAAGCTT CACTTCTCAC CCAGCAAGGT TGACTCATCT GCCTCCATGT CTCTGGGGCT	1200
45	TTGCTGTGTC CCTGAAACCT AGCTGGGCTG GTCTTGCTCC CAGCTTGCTT CCCCCTCTC	1260
	GGATGTCCCT TTGCAGGCCC CTGTCTGTCC TCCGGCACCA GTGTCTTGG CTGCCATGGC	1320
	AAGCTCATCA GGGGCTTGTA CCCTGGTCAC CAAGCATGGT AGCAGCTGCC TGCATTGTAT	1380
50	CTCCATCTGG TCACTGCAGG TGCCAACCCT TCATCCCCCA TGTTTCTCTG GGCCATGGAG	1440
	GGCTGACCTC CGTTTCTGGG GAATGTGGCT GAGCTGTGGT AACCAGCTAC ACCCCAGGTG	1500
55	CTCTTTCCAT GGTGGTGCCT GCTCATCTTG CTGATGCAAA CTAGGAAGTT AGGCTGCATC	1560
	TCGGAGTGGC TTTCGCTGGA GAGGTGCTTT GCTGTCTCTC AGACTCAGTC ACTGTGTTCC	1620
60	CTCCCCGCCT CTCTTATCTC CATGGCTGTT TGCAGCTCTC CCAGGTACTT TGGGGTCTGA	1680

GCTGGAATTC CTTTGTGGTT TGCTCTTCTG CTTCTCACTC TTGTATTAAG AAGGATTCCA 1740
 CAAAGGGAGA GTGGCATCCC TGCTGCTGCT GTGCCAGACC AGAGTTTCCT GAGGGGCCCCT 1800
 5 GACCCTAACC CTCCAGCTCA GCCCTGTACA CCGACCCTG TAAATGAGTG GGGTTTGCTG 1860
 ACTGTAATCC CTGACACCAG TAAAACCAA AGGACTCTTG GGGGCTCAGT GTGAGAGCCA 1920
 GGGTTACCTA CTCTGCCAAG TGAGGACAAA CTGCTAGGCT GTATCCCAT AATTTCAGGAT 1980
 10 GAGAAACATT AACAATAAAA ATTTGTAGTA AACATAACCT CATGANGACT AAAAAAAAAA 2040
 AAAAACYG GGGGGGGCCC GTAACCCATT GGGCCCTNG GGGGGNGTT TTAAAATT 2098

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(2) INFORMATION FOR SEQ ID NO: 149:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1847 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TCGACCCACG CGTCCGAAC T GAGCGGCGG CGGAGCCGG TTGGKGTCTG GTCTTCGCGT 60
 30 CGGCCCCGCG GACCAGACG TGCCCCGCG GCGGGGAGAA GATGGTGCK AGCGGCCTCG 120
 GGGCCGCCAC GCGCCGCCAC GAGTGAGCC AGCGGACCG CGGCGTCCG CCGAGCAGCT 180
 GGGCCGGCTG GGGCCGGGC GCGCANTGCC CGCGGGGCG GGGTGAGCT GATCAGAATA 240
 35 ATGTCAGCA TCAACCCCTT GGAGAACCTG AAGGTGTACA TCAGCAGTCG GCCTCCCTG 300
 GTGGTCTTCA TGATCAGCGT AANGCCATG GCCATAGCTT TCCTGACCCT GGGCTACTTC 360
 40 TTCAAAATCA AGGAGATTAA ATCCCCAGAA ATGGCAGAGG ATGGAATAC TTTTCTGCTA 420
 CGGTTCAATG ATTTGGACTT GTGTGTATCA GAGAATGAAA CCTCAAGCA TCTCACAAC 480
 GACACCACAA CTCCGGAAG TACAATGACC AGCGGGCAGG CCGAGCTTC CACCCAGTCC 540
 45 CCCCAGGCC TGGAGGACTC GGGCCGGTG AATATCTCAG TCTCAATCAC CCTAACCCCTG 600
 GACCCACTGA AACCTTTCG AGGTATTCC CGCAACGTCA CCCATCTGTA CTCAACCATC 660
 50 TTAGGGCATC AGATTGGACT TTCAGGCAGG GAAGCCACG AGGAGATAAA CATCACCTTC 720
 ACCCTGCCTA CAGCGTGGAG CTCAGATGAC TGCGCCCTCC ACGTCACTG TGAGCAGGTG 780
 GTATTACAG CCTGCATGAC CCTCACGGCC AGCCCTGGGG TGTCCCCGT CACTGTACAG 840
 55 CCACCGCACT GTGTTCTGA CACGTACAG AACGCCACG TCTGTACAA GATCTTCACA 900
 ACTGCCAGAG ATGCCAACAC AAAATACGCC CAAGATTACA ATCCTTTCTG GTGTTATAAG 960
 60 GGGGCCATTG GAAAAGTCTA TCATGCTTTA AATCCCAAGC TTACAGTGAT TGTTCAGAT 1020

	GATGACCGTT CATTAATAAA TTGTCATCTC ATGCACACCA GTTACTTCCT CTTTGTGATG	1080
	GTGATAACAA TGTTTTGCTA TGCTGTTATC AAGGGCAGAC CTAGCAAATT GCGTCAGAGC	1140
5	AATCCTGAAT TTGTGCCGA GAAGGTGGCT TTGGCTGAAG CCTAATTCCA CAGCTCCTTG	1200
	TTTTTTGAGA GAGACTGAGA GAACCATAAT CCTTGCCTGC TGAACCCAGC CTGGGCCTGG	1260
10	ATGCTCTGTG AATACATTAT CTGCGATGT TGGGTATTTC CAGCCAAAGA CATTTCAGT	1320
	GCCTGTAAC TATTGTGACA TATTTATAAA AATCTATTCA GAAATTGGTC CAATAATGCA	1380
	CGTGCTTTGC CCTGGGTACA GCCAGAGCCC TTCAACCCCA CCTTGGACTT GAGGACCTAC	1440
15	CTGATGGGAC GTTCCACGT GTCTCTAGAG AAGGATTCCT GGATCTAGCT GGTCAACGAC	1500
	ATGTTTTTAC CAAGGTCACA GGAGCATTCG GTCGCTGATG GGGTTGAAGT TTGGTTTGGT	1560
20	TCTGTTTTCA GCCCAATATG TAGAGAACAT TTGAAACAGT CTGCACCTTT GATACGGTAT	1620
	TGCATTTCCA AAGCCACCAA TCCATTTTGT GGATTTTATG TGTCTGTGGC TTAATAATCA	1680
	TAGTAACAAC AATAATACCT TTTCTCCAT TTTGCTTCCA GGAAACATAC CTTAAGTTTT	1740
25	TTTTGTFTTG TTTTGTFTTT TTTGTFTTTT GTTTTCCTTT ATGAAGAAAA AATAAAATAG	1800
	TCACATTTTA ATACTACCAA AAAATGGACA AAAAAAGTCG AGGGGGG	1847
30		

(2) INFORMATION FOR SEQ ID NO: 150:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1569 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

	GACGCTGACG AGAGAAGGCC TCTTCCTTGA GGGTTGGTGC TGTGTTGCAG TGACCGTGGC	60
45	GGATTACGCC AACTCGGATC CGGCGGTCGT GAGGTCTGGA CGAGTCAAGA AAGCCGTAGC	120
	CAACGCTGTT CAGCAGGAAG TAAAATCTCT TTGTGGCTTG GAAGCCTCTC AGGTTCTCTG	180
	AGAGGAAGCT CTTTCTGGGG CTGGTGAGCC CTGTGACATC ATCGACAGCA GTGATGAGAT	240
50	GGATGCCCAG GAGGAAAGCA TCCATGAGAG AACTGTCTCC AGAAAAAGA AAAGCAAGAG	300
	ACACAAAGAA GAACTGGACG GGGCTGGAGG AGAAGAGTAT CCCATGGATA TTTGGCTATT	360
55	GCTGGCCTCC TATATCCGTC CTGAGGACAT TGTGAATTTT TCCCTGATTT GTAAGAATGC	420
	CTGGACTGTC ACTTGCACTG CTGCCTTTTG GACCAGGTTG TACCGAAGCA CTACACGCTG	480
60	GATGCTTCCC TGCCTTTGCG TCTGCGACCA GAGTCAATGG AGAAGCTGCG CTGTCTCCGG	540

GCTGTGTGA TCCGATCTCT GTACCATATG TATGAGCCAT TTGCTGCTCG AATCTCCAAG 600
 AATCCAGCCA TTCCAGAAAG CACCCCCAGC ACATTAAAGA ATTCCAAATG CTTACTTTTC 660
 5 TGGTGCAGAA AGATTGTTGG GAACAGACAG GAACCAATGT GGGAAATCAA CTTCAAGTTC 720
 AAAAAACAGT CCCCTAGGTT AAAGAGCAAG TGTACAGGAG GATTGCAGCC TCCCGTTCAG 780
 10 TACGAAGATG TTCATACCAA TCCAGACCAG GACTGCTGCC TACTGCAGGT CACCACCTC 840
 AATTTCATCT TTATTCCGAT TGTCATGGA ATGATATTTA CTCTGTTTAC TATCAATGTG 900
 AGCACGGACA TGCGGCATCA TCGAGTGAGA CTGGTGTTC AAGATTCCCC TGTCCATGGT 960
 15 GGTCCGAAAC TGCGCAGTGA ACAGGGTGTG CAAGTCATCC TGGACCCAGT GCACAGCGTT 1020
 CGGCTCTTTG ACTGGTGGA TCCTCAGTAC CCATTCTCCC TGAGAGCGTA GTTACTGCTT 1080
 20 CCCATCCCTT GGGGGCAGCC TCGAGTGTAG TCCATTAGTA ATCAGATTCC AGTTTGGACA 1140
 GGTGGCTGG ATTGTATATC TCGTTAGTAA TGTACATGCT CTTCAGGTTT TAGGGCTCCT 1200
 GTTAGGGGAG GGAGAAATGT TGAATCAAGA GGGAAAACAA CTACTATGAT TTATAAACAT 1260
 25 ATTTTAATGT AAAAATTGTC ATTTAAAAGG AGTGGCCCTG TTTTCTGTGT TAAAACCCCA 1320
 TTTGGTGCTA TTGAGTTTGT TCTTTATTCT TTTATCCCAG TGAAAATTGT TGATCTTGCT 1380
 30 GTAGGGAAAA ATTAACTCT TTGAATCTCC AAACAAGGAA GTTTCAGCAT TCCCTTATGG 1440
 ATCAGAGGAA CCTTAGAGGC CTGAAATTGT TGCTTCCAGT TTAGCTGCCC CTCAAATTCA 1500
 AGTGAATATT TTCCCTTCTC CCTTACCCT TCTCCAGAAA TAAAGCAGGT GACAGGGTTT 1560
 35 CAGAATCTT 1569

40 (2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

50 CCCACGCTC CGGAAGGATT GACCAGTTAA CCAACATCTT AGCCCCCATG GCTGTGGCC 60
 AGATTATGAC ATTTGGCTCC CCAGTCATCG GCTGTGGCTT TATTTGGGA TGGAACCTGG 120
 55 TATCCATGTG CGTGGAGTAC GTCCTGCTCT GGAAGTTTA CCAGAAAACC CCAGCTCTAG 180
 CTGTGAAAGC TGGTCTTAAA GAAGAGGAAA CTGAATTGAA ACAGCTGAAT TTACACAAAG 240
 ATACTGAGCC AAAACCCCTG GAGGGAATC ATCTAATGGG TGTGAAAGAC TCTAACATCC 300
 60 ATGAGCTTGA ACATGAGCAA GAGCCTACTT GTGCCTCCA GATGGCTGAG CCCTTCCGTA 360

CCTTCCGAGA TGGATGGGTC TCCTACTACA ACCAGCCTGT GTTCTGGCT GGCATGGGTC 420
 TTGCTTTCCT TTATATGACT GTCCTGGGCT TTGACTGCAT CACCACAGGG TACGCCTACA 480
 5 CTCAGGGACT GAGTGGGTTT CATCCTCAGT ATTTTGATGG GAGCATCAGC TATAACTGGA 540
 ATAATGGGAA CTGTAGCTTT TACTTGGCTA CGTCGAAAAT GTGGTTTGGT TCGGCAGGTC 600
 10 TGATCTCAGG ATTGGCACAG CTTCCTGTTT TGATCTTGTG TGTGATCTCT GTATTTCATGC 660
 CTGGAAGCCC CCTGGACTTG TCCGTTTCTC CTTTTGAAGA TATCCGATCA AGGTTTCATTC 720
 AAGGAGAGTC AATTACACCT ACCAAGATAC CTGAAATTAC AACTGAAATA TACATGTCTA 780
 15 ATGGGTCTAA TTCTGCTAAT ATGTGCCCGG AGACAAGTCC TGAATCTGTG CCCATAATCT 840
 CTGTCAGTCT GCTGTTTGCA GCGTCATTG CTGCTAGAAT CGGTCTTTGG TCCTTTGATT 900
 20 TAACTGTGAC ACAGTTGCTG CAAGAAAATG TAATTGAATC TGAAAGAGGC ATTATAAATG 960
 GTGTACAGAA CTCCATGAAC TATCTTCTTG ATCTTCTGCA TTTTCATCATG GTCATCCTGG 1020
 CTCCAAATCC TGAAGCTTTT GGCTTGCTCG TATTGATTTT AGTCTCCTTT GTGGCAATGG 1080
 25 GCCACATTAT GTATTTCCGA TTTGCCCAAA ATACTCTGGG AAACAAGCTC TTTGCTTGCG 1140
 GTCCTGATGC AAAAGAAGTT AGGAAGGAAA ATCAAGCAAA TACATCTGTT GTTTGAGACA 1200
 30 GTTTAACTGT TGCTATCTG TTAAGTAGAT ATATAGAGCA CATGTGCTTA TTTTGTACTG 1260
 CAGAATCCA ATAAATGGCT GGGTGTTTTG CTCTGTTTTT ACCACAGCTG TGCCTTGAGA 1320
 ACTAAAAGCT GTTTAGGAAA CCTAAGTCAG CAGAAATTAA CTGGATTAAAT TTCCCTTATG 1380
 35 TTGAGGGCCA TGGRAAAAAA ATGGGAAAAA GGAAAACTC AGTTTAAAT ACGGGAGACT 1440
 ATAATGGATA AACTGTRATT CCCCTATTTT TCAATGAGTAG ATACAATCTT ACGTAAAAGA 1500
 40 GTGGTTAGTC ACGTGAATTC AGTTATCATT TGACAGATTC 1540

45 (2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1719 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

55 TACTTATGAG GTCAATTGGA AATAAGAACA CCATTTTACT GGGTCTAGGA TTTCAAATAT 60
 TACAGTTGGC ATGGTATGGC TTTGGTTCAG AACCTGGAT GATGTGGGCT GCTGGGGCAG 120
 TAGCAGCCAT GTCTAGCATC ACCTTTCTCTG CTGTCAGTGC ACTTGTTTCA CGAACTGCTG 180

	ATGCTGATCA ACAGGTGTC GTTCAAGGAA TGATAACAGG AATTCGAGGA TTATGCAATG	240
	GTCTGGGACC GGCCTCTAT GGAATCATTT TCTACATATT CCATGTGGAA CTAAAGAAC	300
5	TGCCAATAAC AGGAACAGAC TTGGGAACAA ACACAAGCCC TCAGCACCAC TTTGAACAGA	360
	ATTCCATCAT CCTTGGCCCT CCTTCCTAT TTGGAGCCTG TTCAGTACTG CTGGCTCTGC	420
10	TTGTTGCCTT GTTTATTCCG GAACATACCA ATTTAAGCTT AAGGTCCAGC AGTTGGAGAA	480
	AGCACTGTGG CAGTCACAGC CATCTCATA ATACACAAGC GCCAGGAGAG GCCAAAGAAC	540
	CTTTACTCCA GGACACAAAT GTGTGACGAC TGAAATCAGG AAGATTTTTC TATCAGCACC	600
15	CAGGTCTTAG TTTTCACCTC TAGTCTGGA TGTACATTCC ATTTCCATCC ACAGTGTACT	660
	TTAAGATTGT CTTAAGAAAT GTATCTGCAT GAACTCCGTG GGAACATAAG GAAGTGGGAA	720
20	CTTAGAACCA GACAGTTTTC CAAAGATGTT ACAATTTCTT TTGAAAAACC TTTTGTATTAT	780
	TAGCACCAAT TTCTYGCCAC TAAGCTATTT GTTTTATTAT ACATCCTTTA ATTAAAACT	840
	ATATATGTAA CTTCITAGAT ATTAGCAAAT GTCTCTGCTA CCATTTCCCTT AAGGTGTTGA	900
25	GCTTTAACTC TATGCTGACT CAGTGAGACA CAGTAGGTAG TATGGTTGTG GACCTATTTG	960
	TTTTAACATT GTAAAATTTT GAGTCAGATT TTAATATTGT AAAATCTTGG GTCAAATAAT	1020
30	TCAAAGCCTT AATGCAGATG CACTAAAACA AAGAAATGGT AAATGAATG TTTGCATTTA	1080
	AAAAAAAAA CTCTTAAGAA AACTGTACTA AATCTGAATC ATGTTTTGAG CTTGTTTGCA	1140
	GTACTTTTAA ACATTATTCA CTACTGTTTT TGAAGTGAGA AAGTATCAGC CATTTAGCAT	1200
35	TTAAGTTGGG GTATTTAGAG CCTGTAATCT AAATGCTGGC TCAAATTTAT TCCCAGCTA	1260
	CTTCTTATAC CACTATTCTT TTAATGTTTG CATAATCATA AGCACCTCAA CACTTGAATA	1320
40	CATAATCTAA AAATTATATA GTAAAGCTGG TAGCCTTGAA AATGTCAGTG TGATATCTAT	1380
	TATGTAGATA AATATATATA GTGCCTTTC AGGACTGTCA CAGTAACACT TTATTTACAG	1440
	AGCTAATGTT TGTCTTAAAT TTTCAGGACC CTAGAGGAGA GCTTTATACA ATTACCGATG	1500
45	TGAATTTCTC TAAAGTGTAT ATTTTGTGT CCAGTTATAT TATTTAAAAA AGTGTTACTT	1560
	TGTAAAAATT GTATATAAAG AACTGTATAG TTTACACTGT TTTTCATCTG TGTGTGGTTA	1620
50	TTGCTTAATG CTTTAAAC TTGGAACACT CACTATGGTT AAATAAGGTC TTAAGAGAA	1680
	TGTAAATATT YGTTAATAA AGTTAAATAT TTTAATGAT	1719

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(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 863 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

5
GGCACGAGGG AAGCCGGGAC GATGTCCGCA TGACAACCGA CGTTGGAGTT TGGAGGTGCT 60
TGCCCTTAGAG CAAGGGAAAC AGCTCTCATT CAAAGGAACT AGAAGCCTCT CCCTCAGTGG 120
10 TAGGGAGACA GCCAGGAGCG GTTTTCTGGG AACTGTGGGA TGTGCCCTTG GGGGCCCGAG 180
AAACAGAAG GAAGATGCTC CAGACCAGTA ACTACAGCCT GGTGCTCTCT CTGCAGTTCC 240
TGCTGCTGTC CTATGACCTC TTTGTCAATT CCTTCTCAGA ACTGCTCCA AAGACTCTTG 300
15 TCATCCAGCT TGTGCTCTTC ATCATCCAGG ATATTGCAGT CCTCTTCAAC ATCATCATCA 360
TTTTCTCAT GTTCTTCAAC ACCTTCGTCT TCCAGGCTGG CCTGGTCAAC CTCCTATTCC 420
20 ATAAGTTCAA AGGGACCATC ATCCTGACAG CTGTGTACTT TGCCCTCAGC ATCTCCCTTC 480
ATGTCTGGGT CATGAACTTA CCTGGAAAA ACTCCAACAG CTTTATATGG ACAGATGGAC 540
TTCAAATGCT GTTTGTATTC CAGAGACTAG CAGCAGTGTG TACTGCTAC TTCTATAAAC 600
25 GGACAGCCGT AAGACTAGGC GATCCTCACT TCTACCAGGA CTCTTTGTGG CTGCGCAAGG 660
AGTTCATGCA AGTTCGAAGG TGACCTCTTG TCACACTGAT GGATACTTTT CCTTCCTGGA 720
30 TAGRAGGCCA CATTTGCTGC TTTGCAGGGG AGAGTTGGGC CCTATGCATG GGGCAAAACA 780
GGTGGGATTT TCCAAGGGAA GGGTTCAGAA TTAGGCTGTG TGTTCAGCC ATTTCCAAGG 840
AAGGGGAAGG GTTTCCTTNC CCT 863
35

(2) INFORMATION FOR SEQ ID NO: 154:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

50 AACAGCAAAA AAGAATGATT TCTTCTGAAA TTGTGGAACA TGAGGATTCA AGTTTTTATT 60
TTGTTACTAG GTGCTGGAGG AACATCCAG TTCACAAAGC CCCCATCTCT TCCTCTGGAG 120
CCAGAGCCTG CGGTGGAATC AAGTCCAAC GAAACATCAG AACAAATAAG AGAGAAATAA 180
55 GAATAGAATG AATGACCCCA AAATARGGTT TTCTTGGCG AGGATGTGCT GGATTAGGAA 240
AGGTGACATG ACACAGGCAG AGCAGAGTGG CACCCACCAC AGAATACAGT GTGTGTTATT 300
ACGAGGAGCC AGCAGTTGAG CCTAAGGTCC TTCTACCTAC CTGGTATTGG CATTTGAGGT 360
60

CGGAAACCCCT CTAAGCCCC ATAAGCCAGG AAAAGTGAAA AGAGAACACA GTTCCTTTAA 420
 GAACTGGCAG CAAGGCTTGA GGCCTTATGT ATGTAGCTGA GTCAGCAAGG TACATGATGC 480
 5 TGTCTGCTTT CAAAAGGACT TTTCTCTCCT AGCTGACTGA CTCCTTCCTT AGTTCAAGGA 540
 ACAGCTGAGA CAGACCTCTG CTGAGTAGCT CTGTGATGAC AAAGCCTTGG TTAACTGAG 600
 GTGATCCTCA GGTGTGTGAGG TTTATTAGTC CCCAAGGCAA ACACAAATAT TAGATTAATA 660
 10 ATCCAACCTT AATAGTATAC ATTTAAAAGA AAAAAACAA AAGCCCTGGA AGNTTGAGGC 720
 CAAGCCTGCT GAGTATTGCA GCTGCATTTG CCCAAAGGGA ATCCAGAACA AGTCCCTCCC 780
 15 TGTATTTTGT TCTTGAGAGG GGTGAGTCTA GAAGCTAGAT CCTATCAGGA TGAGGAGCAG 840
 CAGCCCAGGG CTTGTCTGGA TCAGCACCAA CGATTTTAAA GAAAAAGGA AGAGTTTCTT 900
 AGATGAGTAA TTGTTATTGA AGATAGTCAG TGATAACCAC TGACCAGATG CTATCAATAC 960
 20 ACTATGTGTC CTTTATTAGAA TAAAGATTAC ATATCATCAT TCCTTTGGGG AAAATTGTTA 1020
 TTCAGGTATA AAAACAAGAG ATTATAATAA AAAANTAAAA GAACCCTAAA AAAAAAAAC 1080
 25 CTCGTGCCGA ATTCCCTGCA G 1101

30 (2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2031 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

40 CAATTAACCC GTTGTAGGCC TAGGTTGTTT GGCAAGCCCC NGGCCTAAAG TTTTAATTTCG 60
 GCAGAGCCAA GGCCTGAAA GGAAGGGAAA GGGGAGGGTA GCGGGAGGGT AGCAGGTGAG 120
 TTCCTAGGGC TGAAGGTTT AGCAGCAGCC TGGTGCAGTG CCCTGTCATC AAGACAAACC 180
 45 CACGGTCCTC CTGGGTGCCT ACCAAGCTTG GTTGTACAA AAGCAAGGTG GGAGTCTATT 240
 TTTGTACATG AGATACATCA CACTTACCTG TGGGCCAGTA TTGTGAAGTG AGTCTGAGTT 300
 50 GTTTACACTG ATGCCTTCCC TCCCCACCAC AAATTGTGTA CATAGTCTTC AGAATGATAC 360
 CACCCCTTTC CCCAGCTCCC AACCAAGAGC TGGTTCTAGG CCTGTGTTAT ATGTCATATT 420
 TAGCGTTTTT ATATATGACC TTTGATTCTT GTTGTGTTGA TTTTAGCACA GTGTATGCAC 480
 55 CTTCAATTAA ATACATCTGT GTGCATACAG ATACGCATAT ATGTGTGTGC GTATGCATAT 540
 ATCTCTCATC TGTAGTTTCC AAGAGTTCAG CTGAAGCAGA TGGAGTCCTG CAGCCCAGGA 600
 60 GACACCCTGC ATCCCTGCTA ATAGTGTMTG CCACAAGTAT TAGTGAGTCT TCCTTATTAA 660

	TATTTTCATT TCAGAAGACT GAAGCAAAGC TGATAGTGT TTGCTGTTTCT TTGGCAGCTA	720
5	AGTGAGGGTC TTGGGATGAC TTGCTGTGTT CCTCAAGCTG CACTTTGGGG CCATCTCTGC	780
	AGTATTAAGC CCCCTTTTGG CTGGGTGGTA CTCTGTCTGT GCCTGTGTGT GTGTGTGATA	840
	GTCACTCTTG CATGGCTTCC ATGTCTGGTT TGTGGCATTT GGGGATAAGT GCTGAACCAG	900
10	AGCATTTGCA GTTTGTTTGA GGCTCGTTG CCAATGATAG ATCACTCCTG TTGACCTGGT	960
	ATGTCTGCTT GCTTGCTGCT TTTCCTTGCT TTCTCTTGA AGAGGAAAGG ACTCTGGTCA	1020
15	GGCCAGGCT GAGTGAGATG AGCTGCAGCT GGCTCATGGC CTTCTTAGAG CAGAGAGAGG	1080
	AGTATGTCAT TTTACTAAGT TCCTAAACAA ACATTTATGC AGGCAACACT CCTTGCAGAT	1140
	CCAGAACTG AGGCACAATA GGGTTATGAC TTGCTCAAGA ATATGTAGCT GCTAGGGGGT	1200
20	AAATCAAGGC ATCACAATTT CTGTTTCAGCG GGCAGGAATA GGCTGTGAAT TGCTAGCACT	1260
	TTTTTTTAA GCAATTACTT TTGACTTGT TCCTCTGAAA GTGCAAGAGG CGTACACCTT	1320
25	TCCCAAATGT AGACTAGAAT CTGCAGGATG CCACCCACTG TATAGTTCTG CTTTCCAGA	1380
	GAGGAAGAAC TTTTAGAAAC CAAATGATCT TAATTGTTAT TGCCACCCC TGGCTTTTCC	1440
	GGGTAGAAAA TTCACAGTAG GAATGATTGT TAAGAGAGAG TGCTTGGAAC CATGGGTAA	1500
30	CAGGAAAGGC TACCTAACTT CACATATCTG CAACCAGAGC AGCCACCAAG CATTACTTAG	1560
	CAGCAGGAAA ATGATTGTAT TTGAGTTCCT GTGTGTCCAA AACTGAGGCA CCATGTTCTT	1620
35	TGAAACATG CCACCTCAAG GCTGGGCGCG GTGGCTCACA CCTGTAAATC CCAGCACTTT	1680
	GGGAGGCCGA GCGGGCGGA TCACCGAGT CGGGGAGTTT GAGACCAGCC TGGACCAACA	1740
	TGGGAGAAAC CCCATCTCTA CCTAAAAATA CAAATTAGC CGGGCGTGGT GGCATGCGCC	1800
40	TATAATCTCA GCTACTTGGG AGGGYTGAGG CAGGRGAATT GCTTGAACCC RGGANGGCGG	1860
	AGGTTTGCGG TTGAGTTGAG GATCGTGCCA TTGCACTTCC GGGCCTTGGG GCAACAACAG	1920
45	CAAAAAYTCC GTCTTCAAMW MRTGCCGAAT TCGATATCAA GCTTATCGAT ACCGTCGACC	1980
	TCGAGGGGGG GCCCGGTACC CAATTCGCCC TATAGNGATC GTATTACAAT C	2031

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(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

	CCTGCACCCCT GAGCCCTTCA CCCCTCGAG TTCCCCCAG GTTGGCTTCC TTCGATTCCCT	60
	TTTCTTGGTA TCAACGTTTG ATTGGAAGAA CAACCCCTC TTTGTCAACC TCAATAATGA	120
5	GCTCACTGTG GAGGAGCAGC TCGGGCACAG CTCMCCGTYA TGGTCATTGT TACCCCCCAA	180
	GACCGCAAAA ACTCTGTGTG GACACAGGAT GGACCCTCAG CCCAGATCCT GCAGCAGCTT	240
10	GTGGTCCTGG CAGCTGAAGC CCTGCCCATG TTAGAGAAGC AGCTCATGGA TCCCCGGGGA	300
	CCTGGGGACA TCAGGACAGT GTTCCGGCCG CCCTTGGACA TTTACGACGT GCTGATTGCG	360
	CTGTYTCTTC GCCATATCCC GCGGCACCGC AGGCTTGTGG ACTCGCCAGY TGCCTCCTTC	420
15	TGCCGGGGCC TGCTCAGCCA GCCGGGGCCC TCATCCCTGA TGCCCGTGCT GGGTNATGAT	480
	CCTNCTCAGC TCTATCTGAC GCAGCTCAGG GAGGCCTTTG GGGATCTGGC CCTTTTCTTC	540
20	TATGACCAGC ATGGTGGAGA GGTGATTGGT GTCTCTGGA AGCCCAACCAG CTTCCAGCCG	600
	CAGCCCTTCA AGGCCCTCCAG CACAAAGGGG CGCATGGTGA TGTCTCGAGG TGGGAGCTA	660
	GTAATGGTGC CCAATGTTGA AGCAATCCTG GAGGACTTTG CTGTGCTGGG TGAAGGCCTG	720
25	GTGCAGACTG TGGAGGCCCG AAGTGAGAGG TGGACTGTGT GATCCCAGCT CTGGAGCAAG	780
	CTGTAGACGG ACAGCAGGAC ATTGGACCTC TAGAGCAAGA TGTCAGTAGG ATGACCTCCA	840
30	CCCTCCTTGG ACATGAATCC TCCATGGAGG GCCTGCTGGC TGAACATGCT GAATCATCTC	900
	CAACAAAACC CAGCCCCAAC TTTCTCTCTG ATGCTCCAGC ATTGGGGCAG GGCATGGTG	960
	GCCCATGTAG TCTCTGGGC CTCACCATCC CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA	1020
35	GGAACTGAAC CCAGGAGATC CATCCACCTA TTAGCCCTGG GCCTGGACCT CCCTGCGATT	1080
	TCCCCTCTCT TCTTAGTCT TCTTCCAGAA ACAGAGAAGG GGATGTGTGC CTGGGAGAGG	1140
40	CTCTGTCTCC TTCTGTCTGC CAGGACCTGT GCCTAGACTT AGCATGCCCT TCACTGCAGT	1200
	GTCAGGCCTT TAGATGGGAC CCAGCGAAAA TGTGGCCCTT CTGAGTCACA TCACCGACAC	1260
	TGAGCAGTGG AAAGGGGCTA TATGTGTATG AATAGACCAC ATTGAAGGAG CACAATGCCC	1320
45	TCCTGTGTTG ATGCCACTTC CCAGGGTGA GACACTGGAA AAGAACCAG GACAGGAAAG	1380
	GATTGGGTAG GTGAAGGGGT CAGGGGACTG GTAGTCACCC AATCTTGGAG AGGTGCAAAA	1440
50	AGCACTGGGG GCTACCCGTT AGCTGCATCT GCCCTGGCTG TTTGCCCGTT CATGTCACAA	1500
	ACTGCCACTA CTATGTACCT GCAGTGGGGT TGCAGAGATG GGGGAGACTC AAGTCTTACT	1560
	CCCCAGGAGC TCCAGGGCC CAAGGAGGAG AATGCTGCCT CCTTTCAGTC TGGTCTACAC	1620
55	CCACTTTCTG GTAGCCTCTC TGCTTCCTGT AATCTGGCT GTTTTTCAG ACTCAGCTCA	1680
	AATAGTGCCC CTCTTAAGC CCATCCCTCG CCCCAGCCT GAGGTGATCT TTCCCTCCTC	1740
60	TGAACTATTA GAGCAGTTAC TGTCTGTTCA GTTCGTTTGG CAGGCACACA CAGTGGCATA	1800

AATTCTATTG TTTTGAAGTC TGATTTAAAA TTAAATGCA GCTGGGCGTG GTGGCTCATG 1860
 CTTGTAATCC CAACACTTAG GGAGTMAGGR GAATCACTTG ASCYCAGGAG TYCTAGACCA 1920
 5 ATCTGGGCAA MAGAGAGACC CCATCTCTTT TAAATAAAAA GTTAAATTGC TTAAAAA 1980
 A 1981

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(2) INFORMATION FOR SEQ ID NO: 157:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 915 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GAATTCGGCA CGAGCGCGGC CATGGCGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC 60
 GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCCTGGAGG AGATCTCGGC TCCAGTTTCG 120
 25 GAGCGGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCGCTGAA GGTATTTGGC 180
 TACCAGCCAG ATCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAACT GCTGGCTGGG 240
 30 TTGCTGCTGG TCATGGGCCC ACCGATGCTG CAAGAGATCA GTAACCTGTT CTGATTCTG 300
 CTCATGATGG GGGCTATCTT CACCTTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360
 CCAGCCATG TCTGCCTGGG GTTCTGCTG CTGCTGAATG TCGGCCAGCT CTAGCCAG 420
 35 ACTAAGAAG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480
 AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540
 40 ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGT CAGCCAGTGT TGAAAGAGAC 600
 ATTTTGTCTA CCTGGCACTG CTTTCTCTTT TTAGCTTTAC TACTCTTTTG TGAGGAGTAC 660
 ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720
 45 TTAAATCAA CAAAATTCT GATGCCCCAA ATAACCACTT TTAATGCCTT GGTGTAAGTA 780
 TACCTCTGAA CTTTTTCTG TGCCTTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840
 50 AACCATATAT CCTATTTTAT TTCCTCCTTT TAAACCTTA TAACTATAA MAAAAA 900
 AAAAAA CCGA 915

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(2) INFORMATION FOR SEQ ID NO: 158:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2117 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:	
	AGAGCGAAGC GAGGGTGGCG CGGGTCCGGG CATGAAGCTG GGC CGGGCCG TGCTGGGCCT	60
	GCTGCTGCTG GCGCCGTCCG TGGTGCAGGC GGTGGAGCCC ATCAGCCTGG GACTGGCCCT	120
10	GGCCGGCGTC CTCACCGGCT ACATCTACCC GCGTCTCTAC TGCCTCTTCG CCGAGTGCTG	180
	CGGGCAGAAG CGGAGCCTTA GCCGGGAGGC ACTGCAGAAG GATCTGGACG ACAACCTCTT	240
15	TGGACAGCAT CTTGCAAAGA AAATCATCTT AAATGCCGTG TTTGGTTTCA TAAACAACCC	300
	AAAGCCCAAG AAACCTCTCA CGCTCTCCCT GCACGGGTGG ACAGGCACCG GCAAAAATTT	360
	CGTCAGCAAG ATCATCGCAG AGAATATTTA CGAGGGTGGT CTGAACAGTG ACTATGTCCA	420
20	CCTGTTTGTG GCCACATTGC ACTTTCACA TGCTTCAAAC ATCACCTTGT ACAAGGATCA	480
	GTTACAGTTG TGGATTGAG GCAACGTGAG TGCTGTGCG AGGTCCATCT TCATATTTGA	540
25	TGAAATGGAT AAGATGCATG CAGGCCTCAT AGATGCCATC AAGCCTTTCC TCGACTATTA	600
	TGACCTGGTG GATGGGGTCT CTTACCAGAA AGCCATGTTT ATATTTCTCA GCAATGCTGG	660
	AGCAGAAAGG ATCACAGATG TGGCTTTGGA TTTCTGGAGG AGTGGAAAGC AGAGGGAAGA	720
30	CATCAAGCTC AAAGACATTG AACACGCGTT GTCTGTGTCG GTTTTCAATA ACAAGAACAG	780
	TGGCTTCTGG CACAGCAGCT TAATTGACCG GAACCTCATT GATTATTTTG TTCCCTTCCT	840
35	CCCCCTGGAA TACAAACACC TAAAAATGTG TATCCGAGTG GAAATGCAGT CCCGAGGCTA	900
	TGAAATTGAT GAAGACATTG TAAGCAGAGT GGCTGAGGAG ATGACATTTT TCCCCAAAGA	960
	GGAGAGAGTT TTCTCAGATA AAGGCTGCAA AACGGTGTTC ACCAAGTTAG ATTATTTACTA	1020
40	CGATGATTGA CAGTCATGAT TGGCAGCCGG AGTCACTGCC TGGAGTTGGA AAAGAAACAA	1080
	CACTCAGTCC TTCCACACTT CCACCCCCAG CTCCTTTCCC TGAAGAGGA ATCCAGTGAA	1140
45	TGTTCTGTGT TGATGTGACA GGAATTCCTC CTGGCATTGT TTCCACCCCC TGGTGCCTGC	1200
	AGGCCACCCA GGGACCACGG GCGAGGACGT GAAGCCTCCC GAACACGCAC AGAAGGAAGG	1260
	AGCCAGCTCC CAGCCCACTC ATCGCAGGGC TCATGATTTT TTACAAATTA TGTTTTTAATT	1320
50	CCAAGTGTTC CTGTTTCAAG GAAGGATGAA TAAGTTTAT TGAAAATGTG GTAACCTTAT	1380
	TTAAAATGAT TTTTAACATT ATGAGAGACT GCTCAGATTC TAAGTTGTG GCCTTGTGTG	1440
55	TGTGTTTTTT TTTAAGTTCT CATCATTTAT ACATAGACTG TGATGTATCT TTA CTGGAAA	1500
	TGAGCCCAAG CACACATGCA TGGCATTTGT TCCACAGGAG GGCATCCCTG GGGATGTGGC	1560
60	TGGAGCATGA GCCAGCTCTG TCCCAGGATG GTCCCAGCGG ATGCTGCCAG GGGCAKTGAA	1620

GTGTTTAGGT GAAGGACAAG TAGGTAAGAG GACGCCTTCA GGCACCACAG ATAAGCCTGA 1680
 AACAGCCTCT CCAAGGGTTT TCACCTTAGC AACAAATGGGA GCTGTGGGAG TGATTTTGGC 1740
 5 CACACTGTCA ACATTTGTGA GAACCACTCT TTTGAAAGAA AAGTATTTCC AACTTGTGAC 1800
 TTGCCAGTCA CTCCGTTTTG CAAAAGGTGG CCTTCACTG TCCATTCCAA ATAGCCCACA 1860
 CGTGCTCTCT GCTGGATTCT AAATTATGTG AATTTTGCCA TATTAAATCT TCCTCATTGA 1920
 10 TACTATTATT TGTACGTTT AATCAGAATC CCCGAAACCT CCTATAAAGC TTAGCTGCCC 1980
 CTCTGAGGA TGCTGAGAAC GGTGTCTTTC TTTATAAATG CAAATGGCTA CCGTTTTACA 2040
 15 ATAAATTTT GCATGTGCAA AAAAAAAAAA ANAAAAAAAA AAAATCCCGG GGGGGGGCCG 2100
 GTAACCAATT TGNCCCC 2117

20

(2) INFORMATION FOR SEQ ID NO: 159:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TGTTCCCTAA TCCCTTTTCT AAAAAGGGGG GAAATCCGG ATGGATTITA GGGATTGGTC 60
 TGGTGTGAGC TGTGTTTTAT TGCACACCTA AATCCTGATT ATAGGCTTTT CATTTCTCCG 120
 35 CAAAGCCTTT ATTTTGGCAG TTAAGCCAAA TGTGTTTCC AGAAAGTTAG TTATTTTCTC 180
 CTCCTTTCTT CTTTCTTTT CTCCTTTTTC CCCGTCTGAC CCCAAACGTT ATTGTCCAAA 240
 40 CATGACTGGA CAGCAGCTTT TGTTCCTTGA CCTGTAATA TGACAGTCTG CTAATATTGA 300
 CAGAAGGTGC AGTTTTTGGG TTATAGTCGT GATTTTCGCT AATCAATCAT ATTAGCAGGA 360
 45 AAAAAAAGA CTTGTTTCTG TTGTACTTGA GTCTTAAGAA AAAGTGGCCC ATAGTTTAGT 420
 GGACAATTTT CAAAGGCTTT AGTACCACCT GTATTTCAAA ATGGGGGACC CAACTCCCG 480
 GAAGAAACAA GCTCTGAACA GACTACGTC TCAGCTTAGA AAGAAAAAG AATCTCTAGC 540
 50 TGACCAGTTT GACTTCAAGA TGTATATTGC CTTGTATTTC AAGGAGAAGA AGAAAAAGTC 600
 AGCACTTTTT GAAGTGTCTG AGGTTATACC AGTCATGACA AATAATTATG AAGAAATAT 660
 CCTGAAAGGT GTGCGAGATT CCAGCTATTTC CTGGAAGT TCCCTAGAGC TTTTACAGAA 720
 55 GGATGTGGTA CAGCTCCATG CTCCTCGATA TCAGTCTATG AGAAGGGATG TAATTGGCTG 780
 TACTCAGGAG ATGGATTTC TCTTTGGCC TCGGAATGAT ATTGAAAAA TCGTCTGTCT 840
 60 CCTGTTTCT AGGTGGAAG AATCTGATGA GCCTTTTAGG CCTGTTTCAGG CAAATTTGAG 900

TTTTCATCATG GTGACTATGA AAAACAGTTT CTGCATGTAC TGAGCCGCAA GGACAAGACT 960
 5 GGAATCGTTG TCAACAATCC TAACCAGTCA GTGTTTCTCT TCATTGACAG ACAGCACTTG 1020
 CAGACTCCAA AAAACAAAGC TACAACTCTC AAGTTATGCA GCATCTGCCT CTACCTGCCA 1080
 CAGGAACAGC TCACCCACTG GGGCAGTTGG CACCATAGAG GRTCACCTCC GTCCTTATAT 1140
 10 GCCAGAGTAG AGTACTGACC AGCAAAATGG AGAAGATCAG AGAATGCAGC AGCAGTTTTT 1200
 TTTCTTGTTT TCTTACCACT TTATCTTTTC AGAGTTTAAA GAAATGGAC TCATGCACAG 1260
 15 AACACTATGC ATTTTGAAAC TTGTTTCATCC TGGATTTTTT TAAATCATTT TTATCTCAGA 1320
 ACTTAAACAA AAATTAGATG TCGTGCACGG ACTGTGTGAA AGAAGATGCT TTGCATATTT 1380
 GCTGCACTGC ATCAGTATCT TACTAAAAAT GTGAAATGAA AGGACTATMG TACTCTGAAA 1440
 20 TGCTTAAATG TATCTGAAAG CACAAGGTGA TACTCATTTT TATGGTCTTC CCATTTGTGC 1500
 TGGTTTTTGC CTCTTTGACA TCTGTCAICA GTATTTAGAG GGTGAGAAAT GAATGTAACA 1560
 25 GGTATAAATA ACATTTTTTA AAACAATAAC TTTGCTATAA TCACAGTTGT TCCAGAGCAC 1620
 TGTCAGATAC ATTCTAATGA CCAGAACTGG TTTAAAAAA GAAAATACAA CCATGGGAAA 1680
 GAAATCTTAA ATGAAAAACG CATCTCATMG TAGGCATTTT TGCCTCATAT TTTACTGGGC 1740
 30 CATGTTTGTT TCCTGGTACT CATGTATTTT TTTTTCCAG ATCTCTTTCC CCAAGTTGCT 1800
 ATTGTAAGAG TATCTGCTG CGTGTGGATG CAGTTATACA CATTAAGCA GATCTGGAGT 1860
 35 CTGAAGTAGC TATAAAGCAG CTATAAACA GAAATACATG CATAGCTGCA GAAACCATGA 1920
 TAGGTAGAGG ACTTTTCTTT TGGTTTGTT TTGTTTGTGTT TTGTTTGTGTT TTGGTTTGA 1980
 CAGAGAAGAG ATTTTTATTA CAAAGAAAAA AATTCCAGTG AATTGTGCAG AAATGCTGGT 2040
 40 TTTTACACCA TCCTAAAGAA AAACCTTACA AGGGTGTGTT GGAGTAGAAA AAAGGTTATA 2100
 AAGTTGGAAT CTFAAATTGT AAAATTAACC ATMGAGTGT CAAAGTTCTAA AAGCAGAACT 2160
 45 CATTTTGTGC AATGAACATA AGGAAAGACT ACTGTATAGG TTTTTTTTTT TTCTCCTTTT 2220
 AAATGAAGAA AAGCTTTGCT TAAGGGTTGC ATACTTTTAT TGGAGTAAAT CTGAATGATC 2280
 CTACTCCTTT GGAGTAAAAC TAGTGCTTAC CAGTTTCCAA TTGTATTTAG CTCTGGTTG 2340
 50 GAATTTGAAA AAAAAAGAAA AAAAGAAAAA GAAAACCTAA ATAAAATAGG TGAAA 2395

55 (2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2120 base pairs

(B) TYPE: nucleic acid

60 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

5	CCCCGATAC CGCTGACGT AGTGCCAATC ACACCTCTCG CGTCTCGGCG CCTCGGAGGC	60
	TAATGAGGAC GCCTGGCGAA ACGCAGTAAC GGATTTCCGG GTGGACCTTC GCTTTACGGC	120
	TCGTGAGTTC TTCCGCCCAA CCCAGAGGAA GCGGAGAGC AGTTTACGAC AGCGCCGGTC	180
10	GTGTTTACGG CGGCGCCCGC TGC GCGCGCA TGTTCCTCT TTTCTGGTT TCTCAAGAGT	240
	GCTGCTGCTA ACGCGGTCCC CGGCACGCAC CATCTGTTGC CATCCCGCC GCGCGAGGCA	300
15	TTGCAGATTT TGGAAGATGG CAAAGTTCAT GACACCCGTG ATCCAGGACA ACCCCTCAGG	360
	CTGGGGTCCC TGTGCGGTTT CCGAGCAGTT TCGGGATATG CCCTACCAGC CGTTCAGCAA	420
	AGGAGATCGG CTAGGAAAGG TTGCAGACTG GACAGGAGCC ACATACCAAG ATAAGAGGTA	480
20	CACAAATAAG TACTCTCTC AGTTTGGTGG TGGAAGTCAA TATGCTTATT TCCATGAGGA	540
	GGATGAAAGT AGCTTCCAGC TGGTGGATAC AGCGCGCACA CAGAAGACGG CCTACCAGCG	600
25	GAATCGAATG AGATTTGCCC AGAGGAACCT CCGCAGAGAC AAAGATCGTC GGAACATGTT	660
	GCAGTTCAAC CTGCAGATCC TGCCTAAGAG TGCCAAACAG AAAGAGAGAG AACGCATTCG	720
	ACTGCAGAAA AAGTTCCAGA AACAAATTTGG GGTTAGGCAG AAATGGGATC AGAAATCACA	780
30	GAAACCCCGA GACTCTTCAG TTGAAGTTTG TAGTGATTGG GAAGTGAAAG AGGAAATGGA	840
	TTTTCTCTAG TTGATGAAGA TGCCTACTTT GGAAGTATCA GAGCCACAGG ACATTGAGTG	900
35	TTGTGGGGCC CTAGAATACT ACGACAAAGC CTTTGACCGC ATCACCACGA GGAGTGAGAA	960
	GCCACTGCGG ASATNCAAGC GCATCTTCCA CACTGTCAAC ACCACAGACG ACCCTGTCAT	1020
	CCGCAAGCTG GCAAAAATC AGGGGAATGT GTTTGCCACT GATGCCATCC TGGCCACGCT	1080
40	GATGAGCTGT ACCCGCTCAG TGTATTCCTG GGATATTGTC GTCCAGAGAG TTGGGTCCAA	1140
	ACTCTTCTTT GACAAGAGAG ACAACTCTGA CTTTGACCTC CTGACAGTGA GTGAGACTGC	1200
45	CAATGAGCCC CCTCAAGATG AAGGTAATTC CTTCAATTCA CCCCACAACC TGGCCATGGA	1260
	GGCAACCTAC ATCAACCACA ATTTCTCCCA GCAGTGCTTG AGAATGGGGA AGGAAAGATA	1320
	CAACTTCCCC AACCCAAACC CGTTTGTGGA GGACGACATG GATAAGAATG AAATCGCCTC	1380
50	TGTTGCGTAC CGTTACCGCA GTGGNAAGCT TGGAGATGAT ATTGACCTTA TTGTCCGTTG	1440
	TGAGCAGCAT GCGTCATGA CTGGAGCCAA CGGGGAAGTG TCCTTCATCA ACATCAAGAC	1500
55	ACTCAATGAG TGGGATTCCA GGCAGTGTA TGGCGTTGAC TGGCGTCAGA AGCTGGACTC	1560
	TCAGCGAGGG GCTGTCATG CCACGGAGCT GAAGAACAAC AGCTACAAGT TGGCCCGGTG	1620
	GACCTGCTGT GCTTTGCTGG CTGGATCTGA GTACCTCAAG CTTGGTTATG TGTCTCGGTA	1680
60		

CCACGTGAAA GACTCCTCAC GCCACGTCAT CCTAGGCACC CAGCAGTTCA AGCCTAATGA 1740
 GTTTGCCAGC CAGATCAACC TGAGCGTGGA GAATGCCTGG GGCAITTTAC GCTGCGTCAT 1800
 5 TGACATCTGC ATGAAGCTGG AGGAGGGCAA ATACCTCATC CTCAAGGACC CCAACAAGCA 1860
 GGTCATCCGT GTCTACAGCC TCCCTGATGG CACCTTCAGC TCTGATGAAG ATGAGGAGGA 1920
 AGAGGAGGAG GAAGAAGAGG AAGAAGAAGA GGAAGAACT TAAACCAGTG ATGTGGAGCT 1980
 10 GGAGTTTGTG CTTCACCGA GACTACGAGG GCCTTTGATG CTTAGTGGAA TGTGTGTCTA 2040
 ACTTGCTCTC TGACATTTAG CAGATGAAAT AAAATATATA TCTGTTTAGT CTTAAAAAAA 2100
 15 AAAAAAAAAA AAAAAAAAAAN 2120

20 (2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

30 GGAAGCTGAA GTCCTTCCAG ACCAGGGACA ACCAGGGCAT TCTCTATGAA GCTGCACCCA 60
 CCTCCACCCCT CACCTGTRAC TCAGGACCAC AGAAGCAAAA GTTCTCACTC AACTGGATG 120
 CCAAGGATGG GCGCTTGTTT AATGAGCAGA ACTTCTTCCA GCGGGCCGCC AAGCCTCTGC 180
 35 AAGTCAACAA GTGAAGAAG CTGTACTCGA CCCCACTGCT GGCCATCCCT ACCTGCATGG 240
 GTTTCGGTGT TCACCAGGAC AAATACAGGT TCTTGGTGTT ACCCAGCCTG GGGAGGAGCC 300
 40 TTCAGTCGGC CCTGGATGTC AGCCCAAAGC ATGTGCTGTG CAGAGAGGTC TGTGCTGCAG 360
 GTGGCCTGCC GGCTGCTGGA TGCCCTGGAG TTCCTCCATG AGAATGAGTA TGTTCATGGA 420
 AATGTGACAG CTGAAAATAT CTTTGTGGAT CCAGAGGACC AGAGTCAGGT GACTTTGGCA 480
 45 GGCTATGGCT TCGCNTTCCG CTATTGCCCA AGTGGCAAAC ACGTGGCCTA CGTGGGAAGGC 540
 AGCAGGAGCC CTCACGAGGG GGACCTTGAG TTCATTAGCA TGGACCTGCA CAAGGGATGC 600
 50 GGGCCCTCCC GCCGCRGCGA CCTCCAGAGC CTGGGCTACT GCATGCTGAA GTGGCTCTAC 660
 GGGTTTCTGC CATGGACAAA TTGCCTTCCC AAMAMTGAGG ACATCATGAA GCAAAAACAG 720
 AAGTTTGTG ATAAGCCGGG GCCCTTCGTG GGACCCTGCG GTCACCTGGAT CAGGCCCTCA 780
 55 GAGACCTGTC AGAAGTACCT GAAGGTGGTG ATGGCCCTCA CGTATGAGGA GAAGCCGCC 840
 TACGCCATGC TGAGGAACAA CCTAGAAGCT TTGCTGCAGG ATCTGCGTGT GTCTCCATAT 900

60

(2) INFORMATION FOR SEQ ID NO: 162:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GGCACGAGAT GAGGGGCACC CAGTGCTTCT AGGGCAGGCT GGGTGGTGGT CCCCTAGGTA 60
15 TCAGCCTCTC TTA CTGTACT CTCCGGAAT GTTAACCTTT CTATTTTCAG CCTGTGCCAC 120
CTGTCTAGGC AAGCTGGCTT CCCCATTTGGC CCCTGTGGGT CCACAGCAGC GTGGCTGCCC 180
20 CCCAGGGCCA CCGCTTCTTT CTGTATCCTC TTTCCTTAAC AGTGACTTGG GCTTGAGTCT 240
GGCAAGGAAC CTGTCTTTTA GCTTCACCAC CAAGGAGAGA GGTGACATG ACCTCCCCGC 300
CCCCTACCA AGGCTGGGAA CAGAGGGGAT GTGGTGAGAG CCAGGTTCTCT CTGGCCCTCT 360
25 CCAGGGTGTT TTCCACTAGT CACTACTGTC TTCTCCTGT AGCTAATCAA TCAATATTCT 420
TCCCTTGCTT GTGGGCAGTG GAGAGGCTGC TGGGTGTACG CTGCACCTGC CCACTGAGTT 480
GGGAAAGAG GATAATCAGT GAGCACTGTT CTGCTCAGAG CTCCTGATCT ACCCCACCCC 540
30 CTAGGATCCA GGA CTGGGTC AAAGCTGCAT GAAACCAGGC CCTGGCAGCA AACCTGGGAA 600
TGGCTGGAGG TGGGAGAGAA COTGAACCTC TCTTTCCCTC TCCCTCCTCC AACATTACTG 660
35 GAACTCTATC CTGTTAGGAT CTTCTGAGCT TGTTTCCCTG CTGGGTGGGA CAGAGGACAA 720
AGGAGAAGGG AGGGTCTAGA AGAGGCAGCC CTTCTTTGTC CTCTGGGGTA AATGAGCTTG 780
ACCTAGAGTA AATGGAGAGA CCAAAGCCT CTGATTTTAA ATTTCCATAA AATGTTAGAA 840
40 GTATATATAT ACATATATAT ATTTCTTTAA ATTTTGTAGT CTTTGATATG TCTAAAAATC 900
CATTCCTCTT GCCCTGAAGC CTGAGTGAGA CACATGAAGA AAAGTGTTT TCATTTAAAG 960
45 ATGTTAATTA AATGATTGAA ACTTGAAAAA AAAAAAAAAA AAA 1003

50

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2196 base pairs

(B) TYPE: nucleic acid

55

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

60

AAGAAGCGGC ACACGGATGT GCAGTTCTAC ACAGAAGTGG GAGAGATAAC CACGGACTTG 60

	GCGAAACATC AGCATATGCA TGACCGAGAT GACCTCTATG CTGAGCAGAT GGAACGAGAA	120
5	ATGAGGCACA AACTGAAAAC AGCCTTTAAA AATTTCATTG AGAAAGTAGA GGCTCTAACT	180
	AAGGAGGAAC TGGAAATTGA AGTGCCTTTT AGGGACTTGG GATTTAACGG AGCTCCCTAT	240
	AGGAGTACCT GCCTCCTTCA GCCCACTAGT AGTGCCTGG TAAATGCTAC GGAATGGCCA	300
10	CCTTTTGTGG TGACATTGGA TGAGGTAGAG CTGATCCACT TTRAGCGGGT CCAGTTTCAC	360
	CTGAAGAACT TTGATATGGT AATCGTCTAC AAGGACTACA GCAAGAAAGT GACCATGATC	420
15	AACGCCATTC CTGTAGCCTC TCTTGACCCC ATCAAGGAAT GGTGAATTC CTGCGACCTG	480
	AAATACACAG AAGGAGTACA GTCCCTCAAC TGGACTAAAA TCATGAAGAC CATTTGTGAT	540
	GACCCGTAGG GCTTCTTCGA ACAAGGTGGC TGGTCTTTCC TGGAGCCTGA GGGTGAGGGG	600
20	AGTGATGCTG AAGAAGGGGA TTCAGAGTCT GAAATTGAAG ATGAGACTTT TAATCCTTCA	660
	GAAGATGACT ATGAAGAGGA AGAGGAGGAC AGTGATGAAG ATTATTTCATC AGAAGCAGAA	720
25	GAGTCAGACT ATTCTAAGGA GTCATTGGGT AGTGAAGAAG AGAGTGGAAG GGATTGGGAT	780
	GAAGTGGAGG AAGAAGCCCG AAAAGCGGAC CGAGAAAGTC GTTACGAGGA AGAAGAAGAA	840
	CAAAGTCGAA GTATGAGCCG GAAGAGGAAG GCATCTGTGC ACAGTTCGGG CCGTGGCTCT	900
30	AACCGTGGTT CCAGACACAG CTCTGCACCC CCCAAGAAAA AGAGGAAGTA ACTTCTGAAC	960
	TTTGGCCCTG AGCTCCATTC TTCTCCAGC CAACCCCTGA AAATTTTACA TGACATAGAA	1020
35	ACTGTATTTT TCCTTTCTGT TTCATTGAA GTTTTGCCAT TTGTGTTTAT GGGTTTAGGG	1080
	GGCCATTTGT GTGGACCAAT CTAATCGGG AATTCCAGGC CCACCAGGAC ACGTGCCAAT	1140
	GGCCCCATTC AGATGGCAAG GGAGGAGGTG TTCTTGAAGA CAGGAGGAGG CTCCCCTGT	1200
40	TAATAAATAT TGTTTCAITC TTCTCTCTTC CTGTACCTT CTGCCAAGAC ATTGATGGCT	1260
	TCTGACATCT TATTTGGTGT CTCAAAGCTG TATTTCCAAG ACAGTGGTAC AAGGTGACCC	1320
45	TTAATTACCC GTATCATGGT TCTTGACCAG CACATTCAAT CCTCCAACCT ACCCTACTGC	1380
	CATGACCTTC CGCACATCTC TAAGTTTAT CTTTGCAATA CTCAGGTTC TCGGAAATTT	1440
	GCTAATGGTT GTGATAAACC ATACAGCTTG AGCCAGTGAG GCAGATTGGG CTGGTGCCTT	1500
50	CGTCTGAGTT TTCTGCTTT CCTGCCTCGT GCAGATTCTG AGGTATATCT GCTGCCTTGG	1560
	AAGACATAAG AAGCAGTGAT ACTCCCTGGC TCGGTATTTT TCTCCATACA ATGCACACAT	1620
55	GGTACAATGA TAGAAGGCAA AATTGCCACT GTCTTCTTTT TTTTCTCATA TATCTAAGGA	1680
	AGATATATCA GGTGTGCCT CATGTACCGC TTCTAGTGAA ATGTAGAGGA AGGCTCAAAG	1740
	GAGTCAACAT TTAGATCTGG AAGGGACAAG TCATGCCTTG GGCCTAGAAT ACCCTGATGA	1800
60	GAAAAGAGAA GAGGAAGGGA GGCCATATCT ACAACANCAN CCTCTCGGCA CTGCTGCTCC	1860

TTATTTTAAC TTTGTCTTGC ATTGTCCTGT ATTTATCACA GTTCTCTGTG AACAGCTTTT 1920
 CAAGTATTTG GGGAGTTTAT CTTGCCATCC TCCCCTTCTG GTTCTCTGCA CCCACCTGTC 1980
 5 CCACTGCAGT TCCTTCCGTG CTCTGTGACT TTAAGAGAAG AAGGGGGGAG GGTCCCGGA 2040
 TTTTATGTTT GTTTGTTTTT TCTCCTTAGC AGTAGGACTT GATATTTTCA ATTTTGGAAG 2100
 10 AACTAAAAGA TGAATAAACT GGGTTTTTTT TGTGTTTTGT TTTTGTAAAA AAAAAAAAAA 2160
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2196

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(2) INFORMATION FOR SEQ ID NO: 164:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1945 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCACAGAGTC GGGCGGACGG ACAGGGAGAG GAGGAGAGGG GGTCTGCGCG CGGCCGCTAC 60
 CCAGAAGCCA GCGGACGGCA GCACGGAGTG GGCTGTCCCC GAGCCCAGCC CCGAGCGAGC 120
 30 CCCCCCCCCG CCCCCGMAGG ACGCGCCTYC CAGCCAGCCC GACTYCTAGG AGGAGGGGAG 180
 GCGGGAAGC AGCTCAAGCC TCACCCACCG CCTGCCCCC AGCCCCGCCA CTCCCAGGCT 240
 35 CCTCGGACT CGGCGGGTCC TCCTGGGAGT CTCGGAGGGG ACCGGCTGTG CAGACGCCAT 300
 GGAGTTGGTG CTGCTCTTCC TCTGCAGCCT GCTGCCCCC ATGGTCTCTG CCAGTGCAGC 360
 TGAAAAGGAG AAGGAAATGG ACCCTTTTCA TTATGATTAC CAGACCCTGA GGATTGGGGG 420
 40 ACTGGTGTTC GCTGTGGTCC TCTTCTCGGT TGGGATCCTC CTTATCCTAA GTCGCAGGTG 480
 CAAGTGCAGT TTCAATCAGA AGCCCCGGGC CCCAGGAGAT GAGGAAGCCC AGGTGGAGAA 540
 45 CCTCATCACC GCCAATGCAA CAGAGCCCCA GAAAGCAGAG AACTGAAGTG CAGCCATCAG 600
 GTGGAAGCCT CTGGAACCTG AGGCGGCTGC TTGAACCTTT GGATGCAAAT GTCGATGCTT 660
 AAGAAAACCG GCCACTTCAG CAACAGCCCT TTCCCCAGGA GAAGCCAAGA ACTTGTGTGT 720
 50 CCCCCACCCT ATCCCCTCTA ACACCATTC CACACCTGAT GATGCAACTA ACACTTGCCT 780
 CCCCCTGCA GCCTGCGGTC CTGCCCACCT CCCGTGATGT GTGTGTGTGT GTGTGTGTGT 840
 55 GTGACTGTGT GTGTTTGCTA ACTGTGGTCT TTGTGGCTAC TTGTTTGTGG ATGGTATTGT 900
 GTTTGTAGT GAACTGTGGA CTCGCTTTCC CAGGCAGGGG CTGAGCCACA TGGCCATCTG 960
 CTCTCCCTG CCCCCGTGGC CCTCCATCAC CTTCTGCTCC TAGGAGGCTG CTGTGTGCCC 1020
 60

GAGACCAGCC CCCTCCCCTG ATTTAGGGAT GCGTAGGGTA AGAGCACGGG CAGTGGTCTT 1080
 CAGTCGTCTT GGGACCTGGG AAGGTTTGCA GCACTTTGTC ATCATTTCTC ATGGACTCCT 1140
 5 TTTACTCCTT TAACAAAAAC CTTGCTTCCT TATCCACCT GATCCCAGTC TGAAGGTCTC 1200
 TTAGCAACTG GAGATACAAA GCAAGGAGCT GGTGAGCCCA GCGTTGACGT CAGGCAGGCT 1260
 10 ATGCCCTTCC GTGGTTAATT TCTTCCCAGG GGCTTCCACG AGGAGTCCCC ATCTGCCCCG 1320
 CCCCTTCACA GAGCGCCCGG GGATTCCAGG CCCAGGGCTT CTA CTCTGCC CCTGGGGAAT 1380
 GTGTCCCCTG CATATCTTCT CAGCAATAAC TCCATGGGCT CTGGGACCCT ACCCCTTCCA 1440
 15 ACCTTCCCTG CTTCTGAGAC TTCAATCTAC AGCCCAGCTC ATCCAGATGC AGACTACAGT 1500
 CCCTGCAATT GGGTCTCTGG CAGGCAATAG TTGAAGGACT CCTGTTCCGT TGGGGCCAGC 1560
 ACACCGGGAT GGATGGAGGG AGAGCAGAGG CCTTTGCTTC TCTGCCTACG TCCCCTTAGA 1620
 20 TGGGCAGCAG AGGCAACTCC CGCATCCTTT GCTCTGCCCTG TCRGTGGTCA GAGCGGTGAG 1680
 CGAGGTGGGT TGGAGACTCA GCAGGCTCCG TGCAGCCCTT GGAACAGTG AGAGGTTGAA 1740
 25 GGTCAATACG AGAGTGGGAA CTCAACCCAG ATCCCCCCCC TCCTGTCTC TGTGTTCCCG 1800
 CGGAAACCAA CCAAACCGTG CGCTGTGACC CATGTCTGTT CTCTGTATCG TGATCTATCC 1860
 30 TCAACAACAA CAGAAAAAAG GAATAAATA TCCTTTGTTT CCTAGTGAAA AAAAAAAAAA 1920
 AAAAAAAAAA AAAAAAAAAA CTCGA 1945

35

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 2933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

45

GGGTCGACCC ACGCGTCCGG CAGCCGTCGT TTGAGTCGTT GCTGCCGCTG CCCCTCCCG 60
 GATCAGGAGC CAGTGTATAC CGCCGCCCA CGCCTTGGT GCCGCTAGAG GAAACGAGAA 120
 50 GGAGGCCGCC TCGGTTTGT CGCCGAGCT CGCCCMYGY CYGGRAGAGC CGAGCCCCG 180
 CCCAGTCGGT CGCTGCCAC CSCTCTAGC CGTTACCCGC GGGCCGCCAC AGCCGCCGGC 240
 CGGAGAGGC GCGCGCCATG GCTCTGGAG CCGATTCAA AGGTGATGAC CTATCAACAG 300
 55 CCATTCTCAA ACAGAAGAAC CGTCCCAATC GGTAAATTGT TGATGAAGCC ATCAATGAGG 360
 ACAACAGTGT GGTGTCTTG TCCAGCCCA AGATGGATGA ATTGCAGTTG TTCCGAGGTG 420
 60 ACACAGTGT GCTGAAAGGA AAGAAGAGC GAGAAGCTGT TTGCATCGTC CTTTCTGATG 480

	ATACTTGTTTC TGATGAGAAG ATTCCGGATGA ATAGAGTTGT TCGGAATAAC CTTCGTGTAC	540
	GCCTAGGGGA TGTATCAGC ATCCAGCCAT GCCCTGATGT GAAGTACGGC AAACGTATCC	600
5	ATGTGCTGCC CATGTATGAC ACAGTGAAG GCATTACTGG TAATCTCTTC GAGGTATACC	660
	TTAAGCCGTA CTTCCTGGAA GCGTATOGAC CCATCCGGAA AGGAGACATT TTTCTTGTC	720
10	GTGGTGGGAT GCGTGCTGTG GAGTTCAAAG TGGTGGAAAC AGATCCTAGC CCTTATTGCA	780
	TTGTTGCTCC AGACACAGTG ATCCACTGCG AAGGGGAGCC TATCAAACGA GAGGATGAGG	840
	AAGAGTCCTT GAATGAAGTA GGGTATGATG ACATTGGTGG CTGCAGGAAG CAGCTAGCTC	900
15	AGATAAAGGA GATGGTGGAA CTGCCCCGTA GACATCCTGC CCTCTTTAAG GCAATTGGTG	960
	TGAAGCCTCC TAGAGGAATC CTGCTTTACG GACCTCCTGG AACAGGAAAG ACCCTGATTG	1020
20	CTCGAGCTGT AGCAAATGAG ACTGGAGCCT TCTTCTTCTT GATCAATGGT CCTGAGATCA	1080
	TGAGCAAATT GGCTGGTGAG TCTGAGAGCA ACCTTCGTAA AGCCTTTGAG GAGGCTGAGA	1140
	AGAATGCTCC TGCCATCATC TTCATTGATG AGCTAGATGC CATCGCTCCC AAAAGAGAGA	1200
25	AAACTCATGG CGAGGTGGAG CGGCGCATTG TATCACAGTT GTTGACCTC ATGGATGGCC	1260
	TAAAGCAGAG GGCACATGTG ATTGTTATGG CAGCAACCAA CAGACCCAAC AGCATTGACC	1320
30	CAGCTCTACG GCGATTTGGT CGCTTTGACA GGGAGGTAGA TATTGGAATT CCTGATGCTA	1380
	CAGGACGCTT AGAGATTCTT CAGATCCATA CCAAGAACAT GAAGCTGGCA GATGATGTGG	1440
	ACCTGGAACA GTAGCCAATG AGACTCACGG GCATGTGGGT GCTGACTTAG CAGCCCTGTG	1500
35	CTCAGAGGCT GCTCTGCAAG CCATCCGCAA GAAGATGGAT CTCATTGACC TAGAGGATGA	1560
	GACCATTGAT GCCGAGGTCA TGAATCTCT AGCAGTTACT ATGGATGACT TCCGGTGGGC	1620
40	CTTGAGCCAG AGTAACCCAT CAGCACTGCG GGAAACCGTG GTAGAGGTGC CACAGGTAAC	1680
	CTGGGAAGAC ATCGGGGGCC TAGAGGATGT CAAACGTGAG CTACAGGAGC TGGTCCAGTA	1740
	TCCTGTGGAG CACCCAGACA AATTCTGAA GTTTGGCATG ACACCTTCCA AGGGAGTTCT	1800
45	GTTCTATGGA CCTCCTGGCT GTGGGAAAAC TTTGTTGGCC AAAGCCATTG CTAATGAATG	1860
	CCAGGCCAAC TTCATCTCCA TCAAGGTCC TGAGCTGCTC ACCATGTGGT TTGGGGAGTC	1920
50	TGAGGCCAAT GTCAGAGAAA TCTTTGACAA GGCCCGCCAA GCTGCCCCCT GTGTGCTATT	1980
	CTTTGATGAG CTGGATTGCA TTGCCAAGGC TCGTGGAGGT AACATTGGAG ATGGTGGTGG	2040
	GGCTGCTGAC CGAGTCATCA ACCAGATCCT GACAGAAATG GATGGCATGT CCACAAAAA	2100
55	AAATGTGTTT ATCATTGGCG CTACCAACCG GCTGACATC ATTGATCCTG CCATCCTCAG	2160
	ACCTGGCCGT CTTGATCAGC TCATCTACAT CCCACTTCCT GATGAGAAGT CCCGTGTTGC	2220
60	CATCCTCAAG GCTAACCTGC GCAAGTCCCC AGTTGCCAAG GATGTGGAAT TGGAGTTCT	2280

GGCTAAATG ACTAATGGCT TCTCTGGAGC TGACCTGACA GAGATTGACC AGCGTGCTTG 2340
 5 CAAGCTGGCC ATCCGTGAAT CCATCGAGAG TGAGATTAGG CGAGAACGAG AGAGGCAGAC 2400
 AAACCCATCA GCCATGGAGG TAGAAGAGGA TGATCCAGTG CCTGAGATCC GTCGAGATCA 2460
 CTTTGAAGAA GCCATGCGCT TTGCGCGCCG TTCTGTCACT GACAATGACA TTCGGAAGTA 2520
 10 TGAGATGTTT GCCCAGACCC TTCAGCAGAG TCGGGGCTTT GGCAGCTTCA GATTCCCTTC 2580
 AGGGAACCAG GGTGGAGCTG GCCCCAGTCA GGCAGTGA GCGGCACAG GTGGCAGTGT 2640
 ATACACAGAA GACAATGATG ATGACCTGTA TGGCTAAGTG GTGGTGGCCA GCGTGCAGTG 2700
 15 AGCTGGCCTG CCTGGACCTT GTTCCCTGGG GGTGGGGCG CTTGCCAGG AGAGGGACCA 2760
 GGGGTGCGCC CACAGCCTGC TCCATTCTCC AGTCTGAACA GTTCAGCTAC AGTCTGACTC 2820
 20 TGGACAGGGG GTTCTCTGTTG CAAAATACA AAACAAAAGC GATAAAATAA AAGCGATTTT 2880
 CATTTGGTAA AAAAAAAAAA AAAAAAAAAAT CCGGGGGGGG GCCCGAACCA TTT 2933

25

(2) INFORMATION FOR SEQ ID NO: 166:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TOGGAGAGCC GCGGGCGNG CGCCTCTCGG CCAGGAAGCG CCTCTTGGAC GCGTGTNACC 60
 40 GATGCCCAGA AGTGGCCTTG GGCTGGGGAT CACCATAGCT TTTCTAGCTA CGCTGATCAC 120
 GCAGTTTCTC GTGTATAATG GTGTCTATCA GTATACATCC CCAGATTTC TCTATATTG 180
 TTCTTGGCTC CCTGTATAT TTTTCTCAGG AGGCGTCACG GTGGGAACA TAGGACGACA 240
 45 GTTAGCTATG GGTGTTCTG AAAAGCCCCA TAGTGATTGA GTCTTCAAAA CCACCGATT 300
 TGAGAGCAAG GAAGATTTTG GAAGAAAATC TGAAGTGA TTATGACAAA GATTATCTTT 360
 50 TTTCTTAAGT AATCTATTTA GATCGGGCTG ACTGTACAAA TGAAGTCTG AAAAACTCT 420
 TCACCTAGTC TAGAATAGG AGGTGGAGAA TGATGACTTA CCCTGAAGTC TTCCCTTGAC 480
 TGGCGCACT GCGCCTGTC TGTGCCCTG AGCATTCGTC CCAGGCTACG TGGGTTGAG 540
 55 CAGGTGGCAG CTCCCAAGT ATTCGATTTT ATTCATGTA TTAACAAG TTGCCATATT 600
 TCAAAGCCTT GAACTAAGAC TCAATTACCA ACCCGCAGTT TTGTGTCACT GCCCAAAGGA 660
 60 GGTAGGTGA TGGTCTTAA CAAACATGAA GTATGGTGA ATAGGAATAA TATTTATCCA 720

	AAAGATTTTT AAAAATAGGG CTGTGTTTAA AAAAAAAAC AAAACARGAA AAGCAGCAGT	780
	GATTATAGAG AGGTCACACT CTAAGTGGGG TCGCGGCGTG GCCACGCTTC ACGGTCACCC	840
5	TCGTCCGTCC TGCAGTGGCG TGTMTACATG GTCACACGTG TGTGTATCAC CAGTGGGTCA	900
	ACTGCTTGTC ATTCTTCCCG TGGCAGTTTG TGTAGACAAT CTTACTGAGC AAAAGGCAAT	960
10	GAAAAGTCTT GGTTCACACA CTGCGATATA TTGGAATTTT CACCTCAGTT TATGAAGTTT	1020
	ATTTGGAAT CCATAGTCAT CTAAGAATGA ATACCTGTCT GCCATGTATT TCAATCTTAG	1080
	TGAGCCAAAA TTGTTTGTGTT GTTACTACAG AATAGAGATG ACTGTTTTTT GCCACAGCCC	1140
15	TATGGRATTT GCAATCTGTG ATTGCCTTGT AAAAAGGAGA GTGCATATGG CACTGCATTA	1200
	AACGTGTGGT GTTCTAGTC AATGATATTG GTGAGCACAA TGTATTCAAT TAATGGCATA	1260
20	GACCATACCA GACCTAATTT GCAAGTATTG GGTCTTAAAC TTCAAGTGCA ATGTATATGA	1320
	AAACCAATCT GAGCCTTGTA TCTCTTAAAT ATTTATTTTT TTTAACGTGT GAGATGTTCC	1380
	AGAGAAGGTT CTCCATTCAAT TTCAGTGCTG CCTGGAGGAA ACTCGGCAAT GATTTCTTTC	1440
25	AGTTGTGAAG TTCTTTTCGT GTTACACCCT CCCTGAACC CTCAACCTTC GAAATACTCC	1500
	AGTTTTGTGG GTTTGGTCAT TTTTACTTAT AAATTTACCT TTTTGTATTT TGCAATTTAC	1560
30	ATGTGTTTGG TTTGTTTTAA ATTCTGTGAA AGTGGCTTGA TTAAAAGACT CCTTTTAAAT	1620
	GGAAGCCACC AGTCAGCAGA ATGGAAGCTT AGAGGAACCT GCCTGTGAGC GCTGGTCTTT	1680
	GTGTTTGGTT TTGTGATGTA ACGATCTTTG CTGGGGTTTT TTGCTTTGTT TTGAGGGAAA	1740
35	TGTCTTGGAG TAAATTTTAA GTTCTTGGAG TTAATTTGTT TTACAGGAAT TTTGTTTTTT	1800
	AAAAAATAG GATCATTCTG AACTTTGGAA TGACCCCTTT ATATATTTTC TGAAAATGAA	1860
40	AACAGTTACA TGAAAAAAT TTCCAATGAA GATGTCAGCA TTTTATGAAA AACCAGAAGT	1920
	TATTAGATGA AAGCAGCGAG TGAATCTTTA AACAGACTT GATCACGCAC ACACAATAAG	1980
	TCTTCTCTC CGAAACCGGA AGTAAATCTA TATCTGTTAG AAATAATGTA GCCAAAAGAA	2040
45	TGTAAATTTG AGGATTTTTT TGCCAATAGT TTATAGAAAA TATATGAACC AAAGTGATTT	2100
	GAGTTGTAA AAATGTAAAA TAGTATGAAC AAAATTTGCA CTCTACCAGA TTGGAACATC	2160
50	TAGTGAGGTT CACATTCATA CTAAGTTTTT AACATTGTGT TCTTTTGTGA TTCATTTTTT	2220
	ACTTTTATTA AAGGTTCAAA ACC	2243

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(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1816 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

5	GGTGGGNAGC TTTNAAATTTC CCCTTACWGG GCGCCTNTAA GGGGAAACCT TCCCGGAATT	60
	TTCCGGTTCGA CCCACGCGTC CGGCCAGCCT AGGAGAAGAA GTTCGTAGTC CCAGAGGTGA	120
10	GGCAGGAGGC GGCAGTTTCT GGCGGGTGAG GCGGGAGCTG AAGTGACAGC GGAGGCGGAA	180
	GCAACGGTCG GTGGGGCGGA GAAGGGGGCT GGCCCCAGGA GGAGGAGGAA ACCCTTCCGA	240
	GAAAACAGCA ACAAGCTGAG CTGCTGTGAC AGAGGGGAAC AAGATGGCGG CGCCGAAGGG	300
15	GAGCCTCTGG GTGAGGACCC AACTGGGGCT CCCGCCGCTG CTGCTGCTGA CCATGGCCTT	360
	GGCCGGAGGT TCGGGGACCG CTTCGGCTGA AGCATTTGAC TCGGTCTTGG GTGATACGGC	420
20	GTCTTGCCAC CGGGCCTGTC AGTTGACCTA CCCCTTGCAC ACCTACCCTA AGGAAGAAGA	480
	GTTGTACGCA TGTACAGAGG GTTGCAGGCT GTTTTCAATT TGTCAGTTTG TGGATGATGG	540
	AATTGACTTA AATCGAACTA AATTGGAATG TGAATCTGCA TGTACAGAAG CATATTCCCA	600
25	ATCTGATGAG CAATATGCTT GCCATCTTGG KTGCCAGAAT CAGCTGCCAT TCGCTGAACT	660
	GAGACAAGAA CAACTTATGT CCTGATGCC AAAAATGCAC CTACTCTTTC CTCTAACTCT	720
30	GGTGAGGTCA TTCTGGAGTG ACATGATGGA CTCCGCACAG AGCTTCATAA CCTCTTCATG	780
	GACTTTTAT CTTCAAGCCG ATGACGGAAA AATAGTTATA TTCCRGCTA AGCCCAGRAA	840
	TCCCAGGTAC GCACCACATT TGGAGCCAGG AGCCCTACCA AATTTGRGRG RAWCMCTCT	900
35	AAGCAAAATG TCCNTCAKMT CGSMAATGAG AAATTCACAA GCGCACAGGA ATTTTCTTGA	960
	AGATGGAGAA AGTGATGGCT TTTTAAGATG CCTCTCTCTT AACTCTGGGT GGATTTTAAC	1020
40	TACAACTCTT GTCTCTCGG TGATGGTATT GCTTTGGATT TGTGTGCAA CTGTGTGCTA	1080
	CACGCTGTG GACGCAGTAT AGTTTCCCTC TGAGAAGCTG AGTATCTATG GTGACTTGA	1140
	GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTGTGG TTGTTAGATC	1200
45	TAAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC TTGCTCATTC	1260
	TGAAATTTAA GCATTTTCT TTTAAAAGAC AAGTGAATA GACATCTAAA ATTCCACTCC	1320
50	TCATAGAGCT TTTAAAATGG TTTCAATTGA TATAGGCCTT AAGAAATCAC TATAAAATGC	1380
	AAATAAAGTT ACTCAAATCT GTGAAAAAAA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG	1440
	GCCCCGTACC AAKTCGCCCT ATWGTGADTB GTATMTTAT TTTACTAATA TCTGTAGCTA	1500
55	TTTTGTTTTT KGCTTKGGT ATKGTTTTTY TCCCTTYTCT WAGCTATRAG CTGATCATKG	1560
	CYSCCTCTCA CCTCCTGCCA TGATACTGTC AGTTACCTTA GTTACAAGC TGAATATTTA	1620
60	GTAGAAATGA TGCTTCTGCT CAGGAATGGC CCACAAATCT GTAATTTGAA ATTTAGCAGG	1680

AAATGACCTT TAATGACACT ACATTTTCAG GAACTGAAAT CATTAAAATT TTATTTGAAT 1740
AATTATGTGC TGAAAAAAAA AAAAAAAAAA AMWMRARASK RRWWACTCGA GGGGGGGCCC 1800
5 GGTACCCNAT TCGCCG 1816

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(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

AGAAACCGTT GATGGGACTG AGAAACCAGA GTTAAACCT CTTTGGAGCT TCTGAGGACT 60
CAGCTGGAAC CAACGGGCAC AGTTGGCAAC ACCATCAACT TCTCCAAGC AGAGAAACCC 120
25 GAACCCACCA ACCAGGGGCA GGATAGCCTG AAGAAACATC TACACGCAGA AATCAAAGTT 180
ATTGGGACTA TCCAGATCTT GTGTGGCATG ATGGTATTGA GCTTGGGGAT CATTTTGGCA 240
TCTGCTTCCT TCTCTCCAAA TTMTACCCAA GTGACTTCTA CACTGTTGAA CTCTGCTTAC 300
30 CCATTCATAG GACCTTTTTT TTTTATCATC TCTGGCTCTC TATCAATCGC CACAGAGAAA 360
AGGTTRACCA AGCTTTTGGT GCATAGCAGC CTGGTTGGAA GCATTCTGAG TGCTCTGTCT 420
35 GCCCTGGTGG GTTTCATTAT CCTGTCTGTC AAACAGGCCA CCTTAAATCC TGCCTCACTG 480
CAGTGTGAGT TGGACAAAAA TAATATACCA ACAAGAAGTT ATGTTTCTTA CTTTATCAT 540
GATTCACTTT ATACCACGGA CTGCTATACA GCCAAAGCCA GTCTGGCTGG AWCTCTCTCT 600
40 CTGATGCTGA TTTGCACTCT GCTGGAATTC TGCCTAGCTG TGCTCACTGC TGTGCTGCGG 660
TGGAAACAGG CTTACTCTGA CTTCCCTGGG AGTGTACTTT TCCTGCCTCA CAGTTACATT 720
45 GGTAATTCTG GCATGTCCTC AAAAATGACT CATGACTGTG GATATGAAGA ACTATTGACT 780
TCTTAAGAAA AAAGGGAGAA ATATTAATCA GAAAGTTGAT TCTTATGATA ATATGGAAAA 840
GTTAACCATT ATAGAAAAGC AAAGCTTGAG TTTCTTAAAT GTAAGCTTTT AAAGTAATGA 900
50 ACATTAAAAA AAACCATTAT TTCCTGTCA TTAAAGATA ATGTG 945

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(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 902 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5
GGCAGAGCCA CAGGAAGGAT GAGGAAGACC AGGCTCTGGG GGCTGCTGTG GATGCTCTTT 60
GTCTCAGAAC TCCGAGCTGC AACTAAATTA ACTGAGGAAA AGTATGAACT GAAAGAGGGG 120
10 CAGACCCCTGG ATGTGAAATG TGA CTACACG CTAGAGAACT TTGCCAGCAG CCAGAAAGCT 180
TGGCAGATAA TAAGGGACGG AGAGATGCCC AAGACCCCTGG CATGCACAGA GAGGCCTTCA 240
AAGAATTTCC ATCCAGTCCA AGTGGGGAGG ATCATACTAG AAGACTACCA TGATCATGGT 300
15 TTACTGCGCG TCCGAATGGT CAACCTTCAA GTGGAAGATT CTGGACTGTA TCAGTGTGTG 360
ATCTACCAGC CTCCCAAGGA GCCTCACATG CTGTTGATC GCATCCGCTT GGTGGTGACC 420
20 AAGGGTTTTT CAGGGACCCC TGGCTCCAAT GAGAATTCTA CCCAGAATGT GTATAAGATT 480
CCTCCTACCA CCACTAAGGC CTGTGCCCCA CTCTATACCA GCCCCAGAAC TGTGACCCAA 540
GCTCCACCCA AGTCAACTGC CGATGTCTCC ACTCCTGACT CTGAAATCAA CCTTACAAAT 600
25 GTGACAGATA TCATCAGGGT TCCGGTGTTC AACATTGTCA TTCTCCTGGC TGGTGGATTG 660
CTGAGTAAGA GCCTGGTCTT CTCTGTCTG TTTGCTGTCA CGCTGAGGTC ATTTGTACCC 720
30 TAGGCCCACG AACCCACGAG AATGTCTCTT GACTTCCAGC CACATCCATC TGGCAGTTGT 780
GCCAAGGGAG GAGGGAGGAG GTAAAAGGCA GGGAGTTAAT AACATGAATT AAATCTGTAA 840
TCACCRGCTA AAAAAAAAAA AAAAAAACN CGANCCTNNG TTTTCAGCTC CATCAGCTCC 900
35 TT 902

40

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 1883 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

50

AGAAAACAAC TGAAAACCA CTTTTTCTA CACACAGCTG GGGAGGTAGC TGAGAACTTG 60
GCACTGCGCA CACATACTAG GTTGAAAGAG AGTTGAGGAA ACCAGAAGGC CAAGTGGATC 120
55 TGCTGGCAAA CCTGAACCT GTCTCCTGCG CTTGCTCTAC AGTTCTGAAG TTGAAAATCC 180
TTTTTCATGCC TAGCATCTGC TTGAGTTATA AACCCCAAGG CAGCCATGTC ATAGACTAGT 240
GTTTACTCTT GTTTTGACTT TGTTTTAATG CTTCTAAGA CCCAAGTGCC TCCTGCTGTT 300
60

	TCCTCCTTTG TGGTAGCCTC TGGCCATCTG GGACCTCAAT CCCCAGCTTT CCCACTTTCA	360
	GCAGTCCTTT GCTCTCTTTG CTTCTACCTC AAATAGCCCC AGGAGTGGGC TTTAGTCTCC	420
5	AATATGGAGC ATYTCAAGCT TCTCCTGGGG GATGGGGATT GGGATGGGCA GAATCTGTTT	480
	TGGWCTCCG GGTATTTCC AGTGGGTGTA AAAGCAGAGC TGGGCCCTTC CCTCTCTTAT	540
10	CCCTGAGGGT GGGTAAGAAG GACTGTATCT ACACCTGTTT TCCCTACCT TCTCTTTTGT	600
	TAGGGAGGCC TCATTCTAAG TTCCTCAAGA GAGTCTTGG CTAAAGCTG TAGCAAGGGT	660
	GTGCTAGGTG GGGGATTTGG AGCAAAACCG TCGAGTAGGC ATGATACTGG TATGGAGTGG	720
15	GCCTGCAAAA TCAGACAGAA ATGGCTTGAG AAGCCGCAGG GGAGCATGCC TGTCTCTCAG	780
	TGATAGAGTA TGGGAGGGAC CTCCCTAGCT TGGAAAATGA GAATTGAAGG GGTATGAAC	840
20	AAATAGGATG CCTAGTTGAG GATGTTCCCA AAGTTTGTG CAATCTTATC ATTAGTAGAT	900
	TTTATAAGCC ACAGAGACAA ACCAGAAACG GAATAATGTT ACTTTGGATG CTTTATTTTT	960
	TTGTTCTAGG TGTGGCTTTG TACATGCAGA AGAATGCTAT ATGCTGCACA TTTTGCCCTT	1020
25	AAAGTCTTAC GACTTTCCCC ATTTTAGTCT AATGGGAAGA TACAGATGTG CAAGTCTGCT	1080
	TTTTTGTTTT TTGTTATTAT TTTTMTTTT TTGCTCTGTG TTATGGACAT TTTCAGACAT	1140
30	GCACAGAAGT GGAGAGGATG GTCCTTGGAC CCCATGTGTC CATCACCTAG CTGCATCACT	1200
	TATCAGCTAT GGTCAACCTG GTTTCATCTG TATCTCTCTC TTTTCACCTG TATTGTTTAT	1260
	TGAAAATCCA AGACACTATG CCAATGCAAC CGTGACTACT TTGGGAGATT GGTAGTCTCT	1320
35	TTTGATGGTG ATAGTGATGG GGTGCACTAT CATAATCACA TCAGGTCTGC TTTTGTCTTT	1380
	TAATGTTAAC TAATGAAGTT CCAGAGATGG GCCTTAGAAA TGTGTTTTAA GAATTAACAA	1440
40	GGAGTCTCAA AAAGAAATGA GAGGGATGCT TCCTTTCCCC TTGCATCTAC AAAACAAGAG	1500
	AGAGACTGTT CTGTGTAAA ACTCTTTCAA AAATTCTGAT ATGGTAAGGT ACTTGAGACC	1560
	CTTCACCAGA ATGTCAATCT TTTTCTCTGT GTAACATGGA AACTTGTGTG ACCATTAGCA	1620
45	TTGTTATCAG CTGTACTGG TCTCATAACT CTGGTTTGG AAGAATAATT TGGAAATGT	1680
	TGCTGTGTTT TGTGAAAATA ACCTCCCCAA AATAATTAGT AACTGGTTGT TCTACTTGGT	1740
50	AATTTGACAC CCTGTTAATA ACGCAATTAT TTCTGTGTTT TTAAACAGTA TAAATAGTTG	1800
	TAAGTTTGCA TGCATGATGG AAAAAATAAA ACCTGTATCT CTGTTAAAAA AAAAAAAAAA	1860
	AAAAAAAAAA AAAAAAAAAA AAA	1883

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(2) INFORMATION FOR SEQ ID NO: 171:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

	TACTTTTAGA TTTACTGCCT TCAAAAAGTG CCTATTCTGA GCAACATAAA CGTTATTTCCT	60
10	TACATATGTA TGTACACACG GTACCCAGAG TCGTACTGTG GCAGCCTTCA AAAACATACC	120
	ATCAGAAAGA GTAGGTGCTG AGATAAGGNA ACTTTGCCAA ATGNAAGAAA GTCACTCACT	180
15	TCCAATATCC CCTCTTCAAG CGGCTACCGT GRAASGGGCT GCAAACACAT TCCCTGAGCA	240
	TCCCTTGCTG ATACAGCTTC TTTATATTTA TATCCTACTG GATGGTAGCA TATTGCTAAG	300
	GTTTCTGTGA CTCTGCTTCA AGGGAATGTA AGYTTTATGG CATTGAAACA TTTAGGAAAA	360
20	AAAAAGATGT TTAAGAGAAT TAATAGAGCC GTAGTCTGTA TTAGGATGTG TGTCATATGT	420
	GTGTTCTATA AACTAAGCAT CGGTGGGTTT AGAGTGTTAA AGTGTCAGCA CATTCTTCT	480
25	CCTTTTGTCT CTCAGGCTAA CATGAGAGAA AATAGAAAAG TCTTGGCTGT GGGGATTGGA	540
	AGCTCAGGGG GCCAAATGTC CTTGCCAGAT CCTTAGAGCA TTACTTTGAC TCCTAAAAAT	600
	AGTAGTGAT GTTATTTGAT GGCTTTTGTT TCCATAGTTC CATCACTGAC AAAACTGTCA	660
30	ATACTGTTGA TGGAGCAGCA GCATAGCCTA GAGTGATGCA TTCTTACCCA GAGGTGGCAA	720
	TAGGAGAGGG TCCATGTAAA TAGGACGAGG TAGACAGTGC ATGATTGTAG GAGAAGGGTT	780
35	GAAGGGAGGA CATGATTCCA AAAAAGATCG TTCTCAATGT GTCGTCTGAC TCAACCAGCT	840
	GGCAGATTAC ACTTGCCAAG TCGTTCCTTT TCCTTCTAAG TCAGTTGGCT CCATATTAC	900
	TTGAATATGC CTCTGTTTGG GCAAAGCAAG ATACCTCCAC TTAACCTTTA TCCAAGGAAG	960
40	CTCTTGGTGT CCTCTTGGTC ATAAAGTTGT CTCCTACCTA ACCCAGTTTT ACCAAATGGA	1020
	AGTAAAAGGG GACAACTAT GGAAGATGGA CTCCATGCCA TTGCAGTCAG CCACCATTCT	1080
45	CTTTTCCATA TAAGGAGCCC CATTACATAA GCTACGGGTG AGGTTGGAAC AGCTATGTTT	1140
	CATAATTTCA AGAGTGTGAC CACCCTGCTC TAGTCATCAT CATTGATGA ATCCAGTTGA	1200
	CTCTTTGGCA AAAGGGTGAT ACTTTTCACT AAAAATGCCT ACTCTTCCTG TTGATGTTCC	1260
50	TTTTCTGTTT TTACCTTGTC CAATTTCAC ACTAGTCATT TTTTTATTT TTTAGAGGAT	1320
	CAGATTTTAG CGCTGGAAAA TGAGTTCAAA AATTTCAGTG TAATGTCATA AGGATGTTGG	1380
55	GATACAGAGA TTTTTTTTTT CCTTGGAAC AAATGGACTG GGAAGAAACA CAGCATGGCT	1440
	TTGCTCTGAG TTTCAATCTG ATGATTATGA CCATGGAAGA TAGTCTTATG TAAAGGTTAA	1500
	ATGGTGTTTA CAAGTGATA GATAAGGCGG AGATGGTGAG AAGCCGGGTT TTCTCTATGC	1560
60	TAAATGTGTC TACTAAGAGC AGCACTTCCT ACTAGCTAAG CACAATCATA GCCCCACCGT	1620

5 GATGAGCTGC TAGTCTGAAT AACATTCCCT GACTTAGGGA AAGGCACACA AAAACATATA 1680
 AAGAATATGT CTATTTTCAT ATGTGTGATA CTGACAGAGC CATGGTATTC CTAAAATATA 1740
 GGTTCCTCTT TTTTCTTGTA TTCTTAGCAA ATTGCATTTA TTCACTACAT TACAAACCAT 1800
 CACTGATGTA TCCAAATAG CACACATAGT TCAGTATGAA AATAAGAGAA TAAAATCTGT 1860
 10 TATAAGCAAG TGATTTAGGT ATTTTCTTTT GTGTTTATGC ATTATCTGAC TATATTAAAA 1920
 CCTGTTTTTC TATTTACCTT CTATCAGTTT TCTCTACCAA TTATGTTTTT TCAATGCTCT 1980
 ATAAGAATGA ATATGGAAAT TATATTTCTT TTTTCTGTAA AAGAGTTGCA ACTACTTTAT 2040
 15 TATATTTAGA AATCCAATAA ACTTCTTATT ACATTTAAAA AAAAAAAAAA AAAACTCGAA 2100

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(2) INFORMATION FOR SEQ ID NO: 172:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CCTTTGANTG TGGTCCCGGG TGCNGATTGG CAGCGCCTCC GCCGCGGCTC GTGGTTGTCC 60
 CGCCATGGCA CTGTCGCGGG GGCTGCCCGG GGAGCTGGCT GAGGCGGTGG CCGGGGGCCG 120
 35 GGTGCTGGTG GTGGGGGCGG GCGGCATCGG CTGCGAGCTC CTCAAGAATC TCGTGCTCAC 180
 CGGTTTCTCC CACATCGACC TGATTGATCT GGATACTATT GATGTAAGCA ACCTCAACAG 240
 ACAGTTTTTG TTTCAAAGA AACATGTTGG AAGATCAAAG GCACAGGTTG CCAAGGAAAG 300
 40 TGTACTGCAG TTTTACCCGA AAGCTAATAT CGTTCCTAC CATGACAGCA TCATGAACCC 360
 TGAATAAT GTGGAATTTT TCCGACAGTT TATACTGGTT ATGAATGCTT TAGATAACAG 420
 45 AGCTGCCCGA AACCATGTTA ATAGAATGTG CCTGGCAGCT GATGTTCTC TTATTGAAAG 480
 TGGAACAGCT GGTATCTTG GACAAGTAAC TACTATCAA AAGGGTGTGA CCGAGTGTTA 540
 TGAGTGTGAT CCTAAGCCGA CCCAGAGAAC CTTTCCTGGC TGTACAATTC GTAACACACC 600
 50 TTCAGAACCT ATACATGCA TCGTTTGGGC AAAGTACTTG TTCAACCAGT TGTTTGGGGA 660
 AGAAGATGCT GATCAAGAAG TATCTCCTGA CAGAGCTGAC CCTGAAGCTG CCTGGGAACC 720
 55 AACGGAAGCC GAAGCCAGAG CTAGAGCATC TAATGAAGAT GGTGACATTA AACGTATTTT 780
 TACTAAGGAA TGGGCTAAAT CAACTGGATA TGATCCAGTT AAACCTTTTA CCAAGCTTTT 840
 TAAAGATGAC ATCAGGTATC TGTGACAAT GGACAACTA TGGCGGAAAA GGAAACCTCC 900
 60

	AGTTCGGTTG GACTGGGCTG AAGTACAAAG TCAAGGAGAA GAAACGAATG CATCAGATCA	960
	ACAGAATGAA CCCCAGTTAG GCCTGAAAGA CCAGCAGGTT CTAGATGTAA AGAGCTATGC	1020
5	ACGTCTTTT TCAAAGAGCA TCGAGACTTT GAGAGTTCAT TTAGCAGAAA AGGGGGATGG	1080
	AGCTGAGCTC ATATGGGATA AGGATGACCC ATCTGCAATG GATTTTGTCA CCTCTGCTGC	1140
10	AAACCTCAGG ATGCATATTT TCAGTATGAA TATGAAGAGT AGATTTGATA TCAAATCAAT	1200
	GGCAGGGAAC ATTATTCCTG CTATTGCTAC TACTAATGCA GTAATTGCTG GTTTGATAGT	1260
	ATTGGAAGGA TTGAAGATTT TATCAGGAAA AATAGACCAG TGCAGAACAA TTTTMTTGAA	1320
15	TAAACAACCA AACCCAAGAA AGAAGCTTCT TGTGCTTGT GCACTGGATC CTCCCAACCC	1380
	CAATTGTTAT GTATGTGCCA GCAAGCCAGA GGTGACTGTG CGGCTGAATG TCCATAAAGT	1440
20	GACTGTTCTC ACCTTACAAG ACAAGATAGT GAAAGAAAAA TTTGCTATGG TAGCACCAGA	1500
	TGTCCAAATT GAAGATGGGA AAGGAACAAT CCTAATATCT TCCGAAGAGG GAGAGACGGA	1560
	AGCTAATAAT CACAAGAAGT TGTGAGAATT TGGAATTAGA AATGGCAGCC GGCTTCAAGC	1620
25	AGATGACTTC CTCCAGGACT ATACTTTATT GATCAACATC CTTCATAGTG AAGACCTAGG	1680
	AAAGGACGTT GAATTTGAAG TTGTTGGTGA TGCCCCGGA AAAGTGGGGS CCAAACAAGC	1740
30	TGAAGATGCT GCCAAAAGCA TAACCAATGG GCAGTGATGA TGGGAGCTTC AGCCCTCCAC	1800
	CTYCACAGCT TCAAGGAGGC AAGATGGACG TYTCYCATAG TTGATYCGGR TGAAGAAGRT	1860
	TCTCCAATAA TTGCCGACG TTCATGAAG GAAGGAGGAG GAGCCCCGC AAGAGGGGAA	1920
35	TTTAGGNTTG	1930

40 (2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

50	GGCCCTGGCC TCTGGGCTGA GGCTTGCTAG GGAATCGGGG TGGCTCTAAG GGGCAGGGAT	60
	AGGGCTGGGG AGCGCCGGCC TGTGGCCCTG ACCAGCCCTT TCTCGTGCRG GTTCCACCCC	120
55	GATGCAGGTG GTCACGTGCT TGACGCGGGA CAGCTACCTG ACGCACTGCT TCCTCCAGCA	180
	CCTCATGGTC GTGCTGTCTT CTCTGGAACG CACGCCCTCG CCGGAGCCTG TTGACAAGGA	240
	CTTCTACTCC GAGTTTGGGA ACAAGACCAC AGGGAAGATG GAGAACTACG AGCTGATCCA	300
60	CTCTACTCGC GTCAAGTTTA CCTACCCAG TGAGGAGGAG ATGGGGACC TGACGTTTAC	360

	TGTGGCCCAA AAGATGGCTG AGCCAGAGAA GGCCCCAGCC CTCAGCATCC TGCTGTACGT	420
5	GCAGGCCTTC CAGGTGGGCA TGCCACCCCC TGGGTGCTGC AGGGGCCCCC TGCGCCCCAA	480
	GACACTCCTG CTCACCAGCT CCGAGATCTT CCTCCTGGAT GAGGACTGTG TCCACTACCC	540
	ACTGCCCGAG TTTGCCAAAG AGCCGCCGCA GAGAGACAGG TACCGGCTGG ACGATGGCCG	600
10	CCGCGTCCGG GACCTGGACC GAGTGCTCAT GGGCTACCAG ACCTACCCGC AGCCCTCACC	660
	CTCGTCTTCG ATGACGTGCA AGGTCATGAC CTCATGGGCA GTGTCACCCCT GGACCACTTT	720
15	GGGAGGTGC CAGGTGGCCC GGCTAGAGCC AGCCAGGGCC GTGAAGTCCA GTGGCAGGTG	780
	TTTGTCCCCA GTGCTGAGAG CAGAGAGAAG CTCATCTCGC TGTTCGGCTCG CCAGTGGGAG	840
	GCCCTGTGTG GCCGTGAGCT GCCTGTGAG CTCACCGGT AGCCAGGGCC ACAGCCAGCC	900
20	TGTCGTGTCC AGCCTGACGC CTA CTGGGGC AGGGCAGCAG GCTTTTGTGT TCTCTAAAAA	960
	TGTTTTATCC TCCCTTTGGT ACCTTAATTT GACTGTCTC GCAGAGAATG TGAACATGTG	1020
25	TGTGTGTGT GTTAATTCTT TCTCATGTTG GGAGTGAGAA TGCCGGGCCC CTCAGGGCTG	1080
	TGGTGTGCT GTCAGCCTCC CACAGGTGGT ACAGCCGTGC ACACCAGTGT CGTGTCTGCT	1140
	GTTGTGGGAC CGTTGTAAAC ACGTGACACT GTGGGTCTGA CTTTCTCTTC TACACGTCCT	1200
30	TTCTGAAGT GTCGAGTCCA GTCCTTTGTT GCTGTGTGCTG TTGCTGTTGC TGTGCTGTT	1260
	GGCATCTTGC TGCTAATCCT GAGGCTGGTA GCAGAATGCA CATTGGAAGC TCCCACCCCA	1320
35	TATTGTCTT CAAAGTGGAG GTCTCCCCTG ATCCAGACAA GTGGGAGAGC CCGTGGGGC	1380
	AGGGGACCTG GAGCTGCCAG CACCAAGCGT GATTCTGCT GCCTGTATT TCTATTCCAA	1440
	TAAAGCAGAG TTTGACACCG TCAAAAAAAAA AAAAAAAAAA AAAAAAAAAA ATTNCTGCGG	1500
40	CCTCAAGGG	1509

45 (2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 3173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

55	TCGACCCAS GCGTCCGTGC TTTCCACAG AAGGTTAGAC CCTGAAAGAG ATGGCTCAGC	60
	ACCACCTATG GATCTTGCTC CTMTGCCTGC AAACCTGGCC GGAAGCAGCT GGAAAAGACT	120
60	CAGAAATCTT CACAGTGAAT GGGATTCTGG GAGAGTCAGT CACTTTCCCT GTAAATATCC	180

	AAGAACCACG GCAAGTTAAA ATCATTTGCTT GGA CTCTCTAA AACATCTGTT GCTTATGTAA	240
	CACCAGGAGA CTCAGAAACA GCACCCGTAG TTACTGTGAC CCACAGAAAT TATTATGAAC	300
5	GGATACATGC CTTAGGTCCG AACTACAATC TGGTCATTAG CGATCTGAGG ATGGAAGACG	360
	CAGGAGACTA CAAAGCAGAC ATAAATACAC AGGCTGATCC CTACACCACC ACCAAGCGCT	420
10	ACAACCTGCA AATCTATCGT CGGCTTGGGA AACCAAAAAT TACACAGAGT TTAATGGCAT	480
	CTGTGAACAG CACCTGTAAT GTCACACTGA CATGCTCTGT AGAGAAAGAA GAAAAGAATG	540
	TGACATACAA TTGGAGTCCC CTGGGAGAAG AGGGTAATGT CCTTCAAATC TTCCAGACTC	600
15	CTGAGGACCA AGAGCTGACT TACACGTGTA CAGCCCAGAA CCCTGTCAGC AACAAATCTG	660
	ACTCCATCTC TGCCCGGCAG CTCTGTGCAG ACATCGCAAT GGGCTTCCGT ACTCACCACA	720
20	CCGGGTGCT GAGCGTGCTG GCTATGTTCT TTCTGCTTGT TCTCATTTCTG TCTTCAGTGT	780
	TTTTGTTCGG TTGTTCAG AGAAGACAAG ATGCTGCCTC AAAGAAAACC ATATACACAT	840
	ATATCATGGC TTCAAGGAAC ACCCAGCCAG CAGAGTCCAG AATCTATGAT GAAATCCTGC	900
25	AGTCCAAGGT GCTTCCCTCC AAGGAAGAGC CAGTGAACAC AGTTTATTCC GAAGTGCACT	960
	TTGCTGATAA GATGGGAAA GCCAGCACAC AGGACAGTAA ACCTCCTGGG ACTTCAAGCT	1020
30	ATGAAATTGT GATCTAGGCT GCTGGGCTGA ATTCTCCCTC TGGAAACTGA GTTACAACCA	1080
	CCAATACTGG CAGGTTCCTT GGATCCAGAT CTTCTCTGCC CAACTCTTAC TGGGAGATTG	1140
	CAAACGCCA CATCTCAGCC TGTAAGCAAA GCAGGAAACC TTCTGCTGGG CATAGCTTGT	1200
35	GCCTAAATGG ACAAATGGAT GCATACCCCTT CCTGAAATGA CTCCTTCTG AATGAATGAC	1260
	AAAGCAGGTT ACCTAGTATA GTTTTCCCAA ACTTCTTCCC ATCATAGCAC ATGTAGAAAA	1320
40	TAATATTTTT ATGGCACACT GGGATAAACA AGCAAGATTG CTCACTTCTG GAAGCTGCAT	1380
	ATGACTAGAG GCCTCTTGTG ACTGGAGGTA ACAACCCTGC CCAGTAACTG TGGGAGAAGG	1440
	GGATCAATAT TTTGCACACC TGTAATAGGC CATGGCACAC CAGCCAAGAT GCTCTGCTCA	1500
45	CAGTCAGTAT GTGTGAAGAT CCCTGGTGCG TGGCCTTCAC CACGCATCTT GAGCAAATTA	1560
	GGAAAATGTA CCCTTCGCTT GAGGCAGATG CAGCCCTTCC CCCGAGTGCA TGGCTTGGAG	1620
50	AGCAGAATGT GGGCTGCATA TAAGCACACT CATCCCTTTG TCTGGGAATC TTTGTGCAGG	1680
	GCATAACAGG CTTAGTAAGT CCAAACACAG ATGACAGTGC TGTGTGGGTC TCTGTCAAG	1740
	TTGTGGCTCT CAGCCATGTA GACACACTCT CCAAATGGAG TGTGGAAAA TGTCTTTCT	1800
55	GCAGGGTCTA GAGACTGCTG GGACACTTTT CTTGGAGTGC TACTTCAGAA GCCTTATAGG	1860
	ATTTTCTTTT TGGCCAAGAT TTCTTCTGT ATCACTCCAA GCAGCTCAG CAGAAGAAGC	1920
60	AGCCATGCCC AGTATTCCCA CTCTCCAAAA GGAAGTGACC AGCTTATATT TCTCACACTT	1980

	CTGGGGAAC T GGGTATAATC CAACCATCAA AATAGAAGAC CTGCAAGAA GCAGAGTCAT	2040
	TCTCCAGAAG GAACTTGGGA GATGATGGTG CAGATGATGA AACTGGGTTC ATCCCAGTTC	2100
5	CAAAGACTCA GAGAAGTAGA GTTTAAGCTG AGGCAGAGTG CCGCCACCCT GGCATGCCCC	2160
	ACAAACAGAT CACCAGCCAG CTTACACAGG CATTAACTCT CCTCAATGAG GAAGAATCAT	2220
10	TCACAACTGA GCAAGACATT CATATGATCA TTTAAGGAAG TGTTTCCCTT ATGTGTTAGC	2280
	AAGTATAATC GGCTAACTCC TAAATCCCAA TGAATAGTCC TAGGCTGGAC AGCAATGGGC	2340
	TGCAATTAGG CAGATAAAGA CATCAGTCCC AGTAAATGAA TCCATAGACT CATCTAGCAC	2400
15	CAACTACCAT TAGCACTATG TTAGGAGCTG CAAGGCCCCA AAGTAGAAGA TGTGCATAAT	2460
	GTCTGCTCTT GTGTAGCTCA GGAGACAAAT CCAGCACAGA CACTACAGTT AACGCTGAAC	2520
20	TGCAGCTGCA AGTAATAGCA TGAACAGTCA GAAAAATACC TTATGAGGGG GCAGGGCTGA	2580
	AGCTGGGCCT TGAAGGATGG ATGAAATTTG GATAGAGAAT GAGGAAGACA GAGGGCCTCC	2640
	AAGTGAGAGA AGCATGAAAA ATGAGCAGGG CCCTGGATCA GTGGGTGTA TTCAGAGCAC	2700
25	CTCTCCAGAT GCACCATGCA TGCTCACAGT CCCTTGCCCTA TGTGTGGCAG AGTGTCCCAG	2760
	CCAGATGTGT GCGCCACCC CATGTCCATT TACATGTCTT TCAATGCCCA CCTCAAAGG	2820
30	TACCTCTTCT GTAAAGCTTT CCTTGGTATC AGGAATCAAA ATTAATCAGG GATCTTTTCA	2880
	CACTGCTGTT TTTTCTCTT TGGTCTTCT ATCACTAAAA CTCATCTCAT TCAGCCTTAC	2940
	AGCATAACTA ATTATTGTG TTCCTCACTA CATTGTACAT GTGGGAATTA CAGATAAACG	3000
35	GAAGCCKGCT GGGGTGGTGG CTCACGCTG TAATCCCAAC ACTTTGGGAG GCCAAGGCAG	3060
	GCGGATCACC TGAGGTCAGG ARTTCGAGAT TARTCTGGCC AACATGGTGA AACCCCATNT	3120
40	NCTACTAAAA TACGAAATTA GCCAGGTGTG GTGGCACACA TCTGTAGTCC CAG	3173

45 (2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

55	AAATTCGGCA CAGCTGAGAG GAGACACAAG GAGCAGCCCG CAAGCACCAA GTGAGAGGCA	60
	TGAAGTTACA GTGTGTTTCC CTTTGGCTCC TGGGTACAAT ACTGATATTG TGCTCAGTAG	120
	ACAACCACGG TCTCAGGAGA TGTCTGATTT CCACAGACAT GCACCATATA GAAGAGAGTT	180
60	TCCAAGAAAT CAAAAGAGCC ATCCAAGCTA AGGACACCTT CCCAAATGTC ACTATCCTGT	240

CCACATTGGA GACTCTGCAG ATCATTAAGC CCTTAGATGT GTGCTGCGTG ACCAAGAACC 300
 5 TCCTGGCGTT CTACGTGGAC AGGGTGTTC AAGGATCATCA GGAGCCAAAC CCCAAAATCT 360
 TGAGAAAAAT CAGCAGCAAT GCCAACTCTT TCCTCTACAT GCAGAAAAC CTGCGGCAAT 420
 GTCAGGAACA GAGGCAGTGT CACTGCAGGC AGGAAGCCAC CAATGCCACC AGAGTCATCC 480
 10 ATGACAACFA TGATCAGCTG GAGGTCCACG CTGCTGCCAT TAAATCCCTG GGAGAGCTCG 540
 ACGTCTTTCT AGCCTGGATT AATAAGAATC ATGAAGTAAT GTCCTCAGCT TGATGACAAG 600
 15 GAACCTGTAT AGTGATCCAG GGATGAACAC CCCCTGTGCG GTTTACTGTG GGAGACAGCC 660
 CACCTTGAAG GGAAGGAGA TGGGAAGGC CCCTTGCAGC TGAAAGTCCC ACTGGCTGGC 720
 CTCAGGCTGT CTATTCCGC TTGAAAATAG CCAAAAAGTC TACTGTGGTA TTTGTAATAA 780
 20 ACTCTATCTG CTGAAAGGC CTGCAGGCCA TCCTGGGAGT AAAGGGCTGC CTTCCCATCT 840
 AATTTATGT GAAGTCATAT AGTCCATGTC TGTGATGTGA GCCAAGTGAT ATCCTGTAGT 900
 25 ACACATTGTA CTGAGTGGT TTTCTGAATA AATTCCATAT TTTACCTAAA AAAAAAAAAA 960
 AAAAAGTGA GGGGGGGCCC GTACCCAATT T 991

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(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

40

ACAGCCCTCT TCGGAGCCTG AGCCCGGCTC TCCTCACTCA CCTCAACCCC CAGGCGGCCC 60
 CTCCACAGGG CCCCTCTCCT GCCTGGACGG CTCTGCTGGT CTCCCCGTCC CCTGGAGAAG 120
 45 AACAAGGCCA TGGGTGGGCC CTGCTGCTG CCCCTCTGTC YCCTGCTGCW GCCGCCAGCA 180
 TTTCTGCAGC CTRGTGGCTC CACAGGATCT GGTCCAAGCT ACCTTTATGG GGTCACTCAA 240
 CCAAAACACC TCTCAGCCTC CATGGGTGGC TCTGTGGAAA TCCCCTTCTC CTTCTATTAC 300
 50 CCCTGGGAGT TAGCCAYAGY TCCCRACGTG AGAATATCCT GGAGACGGGG CCACTTCCAC 360
 GGGCAGTCCT TCTACAGCAC AAGGCCGCCT TCCATTCA CA AGGATTATGT GAACCGGCTC 420
 55 TTTCTGAACT GGACAGAGGG TCAGGAGAGC GGCTTCCTCA GGATCTCAAA CTGCGGAAG 480
 GAGGACCAGT CTGTGTATTT CTGCCGAGTC GAGCTGGACA CCCGGAGATC AGGGAGGCAG 540
 60 CAGTTGCAGT CCATCAAGGG GACCAAATC ACCATCACCC AGGCTGTAC AACCACCACC 600

ACCTGGAGGC CCAGCAGCAC AACCACCATA GCCGGCCTCA GGGTCACAGA AAGCAAAGGG 660
 CACTCAGAAT CATGGCACCT AAGTCTGGAC ACTGCCATCA GGGTTGCATT GGCTGTCGCT 720
 5 GTGCTCAAAA CTGTCAATTTT GGGACTGCTG TGCTCTCTCC TCTGTGGTGG AGGAGAAGGA 780
 AAGGTAGCAG GGCGCCAAGC AGTGACTTCT GACCAACAGA GTGTGGGGAG AAGGGATGTG 840
 TATTAGCCCC GGAGGACGTG ATGTGAGACC CGCTGTGAG TCCTCCACAC TCGTTCCCCA 900
 10 TTGGCAAGAT ACATGGAGAG CACCTGAGG ACCTTTAAAA GGCAAAGCCG CAAGGCAGAA 960
 GGAGGCTGGG TCCTGAATC ACCGACTGGA GGAGAGTTAC CTACAAGAGC CTTTCATCCAG 1020
 15 GAGCATCCAC ACTGCAATGA TATAGGAATG AGGTCTGAAC TCCACTGAAT TAAACCACTG 1080
 GCATTTGGGG GCTGTTYATT ATAGCAGTGC AAAGAGTTCC TTTATCCTCC CCAAGGATGG 1140
 AAAATACAAT TTATTTTGCT TACCATACAC CCCTTTTCTC CTCGTCCACA TTTTCCAATC 1200
 20 TGTATGGTGG CTGTCTTCTA TGGCAGAAGG TTTTGGGGAA TAAATAGCGT GANATGNTNC 1260
 TGACTIONAAAA AAAAAAAAAA AAAAACTCGA 1290

25

(2) INFORMATION FOR SEQ ID NO: 177:

30

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TGGGGCCCCCT TTTGGATGCT CTGGGTGTTT TTGCCAAGAG TTACAGGATG TCAAGTGTGG 60
 40 GGAGCTCAGC ACCCTTGCTG TGGACCAAGT AAGGCTGTTT CAGACCAGGT GCTTCCAGAC 120
 ATTTCCAGGC TCCAGGAGAG AGGCTGGGAG CCCCCACAGA AAGCACAGGA AAATGCAAAA 180
 45 AAAAAACAGT CTTTTTTTTT TTTTGTCTTT TTATTATGAA AACAAAACAA ATGCCCCAGG 240
 AGAAGGGTCC ATGATTACCA GAAACATCAA AGAGTACTTT CTACCATTTT TATTCTGTTG 300
 TGTGAGGCC AGCATTGCAA TAAACAAGCT AAATACTTA CATTGGACTC ATTTTCAGTA 360
 50 ACTGACATTT ACAGGAATAT ACTAGAAACG GCACTAAAAA GTTTAAGAAA AGTTACGGTA 420
 AACTTGCAATG CACATCATAC AGAAAAGTAA CATTTTAAAT ATAAAAAGA AAAACTTCCT 480
 GGAAGCATTA TGCCAGTATT AAGGAACAGT GCTACTCTGG ATGTGACAAA TTCTGTATGT 540
 55 GGTGTTACT CTTTCCCAA AGACTGTCAG AGGCGTGAGT GCTGCAAAAG AACACAACA 600
 AAAACAACA CACAAAAAA TGTGTCTTAC AGTTTGTAAG CAAGATGACA CTGCCCAACA 660
 60 CAAAGAGGGG TCTGGAGTTC AGTTACGCC CGAAGCCTGC CCCCTCGGCC TCCAGGGGTC 720

	ATTCAGAGTG TTCTCAAATC CAATTCCGAC ACACGACTTG TCACTACTCC TCTCCCCTTG	780
5	AAAAAAGCAT GTTAGAAGCT GCCCTACAGG TCTCAGCAGT GGGACAATCT AATTGAATCA	840
	CCGCAGCCTT CTAATACAGA AGAAACGGAC GTGACTGTCA CCCTCAGCCC GCCAGCAAGG	900
	GCGCTGAGGA AGTCATTAAT CCTTCGAAAC TCTGAAAAGA AACCAGTGTT GAAGTCTGGA	960
10	CAGAAAGCCT TAAAAAAGTG ACAGCACCAA TGCAGCTGCT CAGTGTACCC NCCGTGGGCT	1020
	GTCAGGGTCA GTGGCTTCTT TCTAGATGAA AGGAGCAGAG GCGAGCCGAC GCCACCGTCA	1080
15	CAGAGAACCA GCGAGAAGG AAAGGCCCCA CGATGCTCCC TGTGCGCTGC CCCCACAGCC	1140
	GGCCGCTCCC CCGACGGCTC ACACAGGCAG CACCTCACTG CCCTGTGGCT GGAGGGGCAT	1200
	TGCAAGGAGC GCGCCCGAGC CCCAGGCACC CCGGCTTAG GGTGTACGTA TCACCCAGCC	1260
20	CTGTGCTGGC AGCACGTTAC CAACCAGCCT GCGTGAAGAC CTGTCAACTG TCGTGTGTGA	1320
	ATTCCTTAAA TTCGGTTTAA ATAGTCCATT AAAGATCTGT TTAGAAAATA CCTTTGAAAA	1380
25	CGAGGGTAAC TTTAAAAAAT GGAACTTTC AAATCCATTT ATATTTTAT TATAAACAAA	1440
	ACTTAATTAA AAGTTTAACA AACTGGCTGA AAATCACCA AGTGTACAGC TCACCAGCAA	1500
	TTTAAAAAAT GATAATTTAC CAGCATCTCC TCATCAGAGT TCCCTCTCCA GTAAGGGTAT	1560
30	ACCTACATCT GTAAGGGTCA GTGGACTCTG AATCAATTTT ATGGTTGTTT TAAAATCACC	1620
	GTGTATTAGG ATACTAATGA TAGTCCCTAT ATCCATCCAG AAATGCTGGC AGAAAGCACT	1680
35	GGCCACCATA CAGGACAGAC CACACCACAG CTCCATACCC AGCGTCTGCC TGGAGGCTCC	1740
	CCCACGCTGA GGTCCGGGAG AATGCCTGGT TTCAGTCATT TCCGACTAA CTGTGACAAC	1800
	GCGTGAGCAG GGAGCACCGT GCGAGTCTCC GGGAGGGAAT CCTCCTGGGG CCCAGAGACT	1860
40	CCTCCACCCC TGGGGAGGGC AGACAGGCTC GGGARGGCCT GGCCAGGCCA CTGGAGGCTG	1920
	GCAGGGAGCA GGCATGTCCA CCCGCAAGCC TGGGAGGCTA ACTCTGGCAT TCCTGGCCCG	1980
45	AGCCGCCATG CTCATTGGTG GGCCAGTTTG GGACATCCCC GTACTCAAAG ACCATATGGC	2040
	AGCCTCTGGG AAAACAAAAC CAAAACATCA CCTTCTATTA AACTCTGTAT ATTATTATTT	2100
	TTTACAATAG AAAGTTAAAA ATCAAGACTT AGATTTACTA TACATTTTTT CTCTCAGATT	2160
50	ACAAAGTTTA TATTATATAA CTGGGGTTCC CTAAATGAT TTCPTTTAAA ACAGTCTTAA	2220
	AGAGACCAGA AGTGAATACA AAAGAACTAA ACAAATAAAA AAATTAGAAT GTGCTGTAGC	2280
55	TGAAAGCTGT	2290

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

GGCACGAGCC ATGCCTGGCC TCTCCTTGAT TCTTACAGTC ACTTTGTTGG CTGTTTCTGA 60
CTCAGCAGCT ACCTGCATTG TGGCCAAAGG ATGACCTATT CCTTCTCAGG AGGGCAAAAA 120
TGTGGAATAG TGTCTGTCCA TGCCTCTCCT CATGGGCTAC CACCTCTGCC ACCGTGGTTA 180
ATCAGTAACA ACCAGGAGAG AAGCTGCTGG AACTGACCTC TGGGAACTCC CTGGGATGGT 240
TTGGTGCAGG AATGTAGTAG GCATACACGT GGTTCGCTGG ATCTGGGCCC TCCTGATGTG 300
AGTAGAGAGG TAAAAGGCCA CCATCTCCTT GACCTCTGGG GAACTCATCC ACAAAGAAGA 360
TGTTCCTCAAG ATGCTTCTGA AGATTGCCTA AAAATAGCCG GTTCCACCC CCGTGAATGC 420
ATCCATTCTA GAATGCTCCT TCACCAGGAC CAGAGAACTG ATTTACAGAA GTGACATGAA 480
AACATTCCAT CCCAGAATTT GCAGTAGCTC AAATTAAGTT TCTAGCTATT AAAAAGAAAA 540
AAAAAAAAA 549

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(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

40

GGCACGAGGG CTCATTCAAT CCGCGCGGG CCTGCCAGAC ACCTGCGCCC TTCTGCAGCC 60
GCCCCCGCA TCCGCCGCG CAGCCCCAG CATGTGCGGC CCAGACGTCG AGACGCCGTC 120
CGCCATCCAG ATCTGCCGGA TCATGCGGCC AGATGATGCC AACGTGGCCG GCAATGTCCA 180
CGGGGGGACC ATCCTGAAGA TGATCGAGGA GGCAGGCGCC ATCATCAGCA CCCGGCATTG 240
CAACAGCCAG AACGGGGAGC GCTGTGTGGC CGCCCTGGCT CGTGTGAGC GCACCGACTT 300
CCTGTCTCCC ATGTGCATCG GTGAGGTGGC GCATGTCAGC GCGGAGATCA CCTACACCTC 360
CAAGCACTCT GTGGAGGTGC AGGTCAACGT GATGTCCGAA AACATCCTCA CAGGTGCCAA 420
AAAGCTGACC AATAAGGCCA CCCTGTGGTA TGTGCCCTG TCGCTGAAGA ATGTGGACAA 480
GGTCTCGAG GTGCTCTCTG TTGTGTATTC CCGGCANGAG CAGGAGGAGG AGGGCCGGAA 540
GCGGTATGAA GCCCAGAAGC TGGAGCGCAT GGAGACCAAG TGGAGGAACG GGGACATCGT 600

55

60

	CCAGCCAGTC CTCAACCCAG AGCCGAACAC TGTCAGCTAC AGCCAGTCCA GCTTGATCCA	660
5	CCTGGTGGGG CCTTCAGACT GCACCCTGCA CGGCTTTGTG CACGGAGGTG TGACCATGAA	720
	GCTCATGGAT GAGGTGCGCG GGATCGTGCC TGCACGCCAC TGCAAGACCA ACATCGTCAC	780
	AGCTTCCGTG GACGCCATTA ATTTTCATGA CAAGATCAGA AAAGGCTGCG TCATCACCAT	840
10	CTCGGGACGC ATGACCTTCA CGAGCAATAA GTCCATGGAG ATCGAGGTGT TGGTGGACGC	900
	CGACCCTGTT GTGGACAGCT CTCAGAAGCG CTACCGGGCC GCCAGTGCCT TCTTCACCTA	960
15	CGTGTCGCTG AGCCAGGAAG GCAGGTCGCT GCCTGTGCCC CAGCTGGTGC CCGAGACCGA	1020
	GGACGAGAAG AAGCGCTTTG AGGAAGGCAA AGGGCGGTAC CTGCAGATGA AGGCGAAGCR	1080
	ACAGGGCCAC GCGGASCYTC AGCCCTAGAC TCCCTCCTCC TGCCACTGGT GCCTCGAGTA	1140
20	GCCATGGCAA CGGGCCAGT GTCCAGTCAC TTAGAAGTTC CCCCCTTGCC CAAAAACCCA	1200
	ATTACATMG AGAGCTGGTG TTGTCTGAAG TTTTCGTATC ACAGTGTTAA CCTGTACTCT	1260
25	CTCCTGCAAA CCTACACACC AAAGCTTTAT TTATATCATT CCAGTATCAA TGCTACACAG	1320
	TGTTGTCCCG AGCGCCGGA GCGTTGGGC AGAAACCTC GGAATGCTT CCGAGCACGC	1380
	TGTAGGGTAT GGAAGAACC CAGCACCCT AATAAGCTG CTGCTTGGCT GGAAAAAAA	1440
30	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1500
	AGAAAAAAN	1509

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(2) INFORMATION FOR SEQ ID NO: 180:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

	AGCTGTATCA TAGGAAAGAT GGCCACACCG GCGGTACCAG TAAGTGCTCC TCCGGCCACG	60
50	CCAACCCAG TCCGGCGGC GGCCACAGCC TCAGTTCCAG CGCCAACGCC AGCACCAGCT	120
	GCGGCTCCGG TTCCCGCTGC GGCTCCAGCC TGCATCCTCA GACCTGCGG CAGCAGCGC	180
	TGCAACTGCG GCTCCTGGCC AGACCCCGGC CTCAGCGCAA NTCCAGCGCA GACCCAGCG	240
55	CCCGCTCTGC CTGGTCCTGC TCTTCCAGGG CCTTCCCCG GCGGCCGCGT GGTGAGGCTG	300
	CACCCAGTCA TTTTGGCCTC CATGTGGAC AGCTACGAGA GACGCAACGA GGGTGCTGCC	360
60	CGAGTTATCG GGACCCTGTT GGAAGCTGTC GACAAACACT CAGTGGAGGT CACCAATTGC	420

	TTTTTCAGTGC CGCACAAATGA GTCAGAAGAT GAAGTGGCTG TTGACATGGA ATTTGCTAAG	480
	AATATGTATG AACTGCATAA AAAAGTTTCT CCAAATGAGC TCATCCTGGG CTGGTACGCT	540
5	ACGGGCCATG ACATCACAGA GCACTCTGTG CTGNATCCAT GAGTACTACA GCCGAGAGGC	600
	CCCCAACCCC ATCCACCTCA CTGTGGACAC AAGTCTCCAG AACGGCCGCA TGAGCATCAA	660
10	AGCCTACGTC AGCACTTTAA TGGGAGTCCC TGGGAGGACC ATGGGAGTGA TGTTCACGCC	720
	TCTGACAGTG AAATACGCGT ACTACGACAC TGAACGCATC GGAGTTGACC TGATCATGAA	780
	GACCTGCTTT AGCCCCAACA GAGTGATTGG ACTCTCAAGT GACTTGCAGC AAGTAGGAGG	840
15	GGCATCAGCT CGCATCCAGG ATGCCCTGAG TACAGTGTG CAATATGCAG AGGATGTACT	900
	GTCTGGAAAG GTGTCAGCTG ACAATACTGT GGGCCGCTTC CTGATGAGCC TGGTTAACCA	960
20	AGTACCGAAA ATAGTTCCCG ATGACTTTGA GACCATGCTC AACAGCAACA TCAATGACCT	1020
	TTTGATGGTG ACCTACCTGG CCAACCTCAC ACAGTCACAG ATTGCACTCA ATGAAAACT	1080
	TGTAAACCTG TGAATGGACC CCAAGCAGTA CACTTGCTGG TCTAGGTATT AACCCAGGA	1140
25	CTCAGAAGTG AAGGAGAAAT GGGTTTTTG TGGTCTTGAG TCACACTGAG ATAGTCAGTT	1200
	GTGTGTGACT CTAATAAACG GAGCCTACCT TTTGTAAATT AAAAAAAAAA AAAAAAACCN	1260
30	SGRGGGGGGG CCCGGTCCCA TTSSCCCTTT NGTAATTCGT NTTACAATCC CCNGGC	1316

35 (2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

45	GGCATGWKCA GACATGACTT CTATTGCCAG GCTGGTCAAG TGGCAGGGTC ATGAGGGAGA	60
	CATCGATAAG GGTGCTCCTT ATGCTCCCTG CTCTGGAATC CACCAGCGGG CTATCTGCCT	120
	TTATGGGGCT GGGGACTAGA ATTGGATGCT TCAAAACCAT CACCTGTTGG CCAACAAGTT	180
50	TGACCCAAAG GTAGATGATA ATGCTCTTCA GTGCTTAGAA GAATACCTAC GTTATAAGGG	240
	CCATTCTATT GGGACCTGAA CTTTGAAGAC CACAMTATTG AAGAGGCGTT GCTTACCYGT	300
55	TGGGGGCCAA GAGGCATGTT ACCAAACATG GYYCARGAAM YTTGGYKGGG AMCARKKKKG	360
	GKKGGGARRM CMRGGGYTTG SCAAWTCSK KGGCMWCCYT TTAGGGTAAR RRGCGCKGTW	420
	ATTAGATTGT GGGTAAAGTA GGATCTTTTG CCCTTGCAAA TTTGCTGCCT GGGTGAATGY	480
60	TGCTTGITCC TTCTCMACCC CTAACCCTAG TAGTTCTCTC ACTAACTTTC TCACTAAGTG	540

AGAATGAGAA CTGCTGTGAT AGGGAGAGTG AAGGAGGGAT ATGTGGTAGA GCACTTGATT 600
 TCAGTTGAAT GCCTGCTGGT AGCTTTTCCA TTCTGTGGAG CTGCCGTTC TAATAATTCC 660
 5 AGGTTTGGTA GCGTGGAGGA GAACTTTGAT GGAAAGAGAA CCTTCCCTTC TGTACTGTTA 720
 ACTTAAAAAT AAATAGCTCC TGATTCAAAG TAAAAA AAAA AAAAAA 777

10

(2) INFORMATION FOR SEQ ID NO: 182:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

GGCACAGATA ACTATGTACA TGTATTCCTT AAATGTTTTT TTAAGTTTTA TATTCTTGGC 60
 25 ACTGGTCTTC AAATGTGTAC ATGTGTGCCA GGGAGCAAAT GCCTTCTTGT TTCTGAAATT 120
 GGTCTTTTAG ACTGTTCCTT TTCCCATCT TCTCACCTCC TGCCCTCCT TCAGGGTACT 180
 TCCGTGGCCA GAACCCCTCC AGGTCAGAGG CAGAAGAGAA GCCTCATGGG TCACAGCAGC 240
 30 AGATGTGGGC TGGAGATCTA TTCATTTGGT TTGGCTTGA ATTTTCTGRA TGGTTTACTT 300
 GATCYTGGA AAGANATATC TTGCCAGGAA AAATGATAGN CCTTGACAAT GTTGAATGAT 360
 35 CCTGCACCAC CTTGAAAGAC ATTCTAATA TGGTTTGTCA GGCAAAGTGG TTAGTAGTCA 420
 TTTGTGGCCT GAGGTAGAAG TCCTCAGAAA TCAGCAGACT TCACTGATAA AATGCTGACT 480
 TGCCCTGGA CTGGGCTCTG TGAGAGTGGC CTCTGCACT GTGCACAGTA GGTGTGAACA 540
 40 CACCACACCT ACAGGGACCA CGTGGTGGC TGTGGACTAG CGGCAAGCT CCCTGCAGGC 600
 CCACTAATAG AATTCAGCTT TTAGCATGGG CTGTTTCATA CTGTTCTGAT GAAACTGATT 660
 45 TGGTTTCTTT CCTCCATACC CTTCTGCAT TTCAGTGTTC TTGTTTAGTT TTCCTGGTTT 720
 TTAATTATAA CTACAAAATA AAATCTTTAG GCTATTCACC TTAGCTTAGT AAAAAAAAAA 780
 AAAAAAACT C 791

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(2) INFORMATION FOR SEQ ID NO: 183:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

5	AAATTGATTA ACAGCTTGAA AGAAGGCTCT GGTTTTGAAG GCCTAGATAG CAGCACTGCC	60
	AGTAGCATGG AGCTGGAAGA ACTTCGGCAT GAGAAAGAGA TGCAGAGGGA GGAAATACAG	120
	AAGCTGATGG GCCAGATACA TCAGCTCAGA TCCGAATTAC AGGATATGGA GGCACAGCAA	180
10	GTTAATGAAG CAGAATCAGC AAGAGAACAG TTACAGGWTG TGCATGACCA AATAGCTGGG	240
	CAGAAAGCAT CCAACAAGA ACTAGAGACA GAACTGGAGC GACTGAAGCA GGAGTTCCAC	300
	TATATAGAAG AAGATCTTTA TCGAACAAAG AACACATTGC AAAGCAGAAAT TAAAGATCGA	360
15	GACGAAGAAA TTCAAAAACCT CAGGAATCAG CTTACCAATA AAACTTTAAG CAATAGCAGT	420
	CAGTCTGAGT TAGAAAATCG ACTCCATCAG CTAACAGAGA CTCTCATCCA GAAACAGACC	480
20	ATGCTGGAGA GTCTCAGCAC AGAAAAGAAC TCCCTGGTCT TTCAACTGGA GCGCCTCGAA	540
	CAGCAGATGA ACTCCGCCTC TGAAGTAGT AGTAATGGGT CTTGATTAA TATGTCTGGA	600
	ATTGACAATG GTGAAGGCAC TCGTCTCGCA AATGTTCTCTG TTCTTTTAA TGACACAGAA	660
25	ACTAATCTGG CAGGAATGTA CGGAAAAGTT CGCAAAGCTG CTAGTTCAAT TGATCAGTTT	720
	AGTATTCGCC TGGGAATTTT TCTCCGAAGA TACCCCATAG CGCGAGTTT TGTAATTATA	780
30	TATATGGCTT TGCTTCACCT CTGGGTCATG ATTGTTCTGT TGAATTACAC ACCAGAAATG	840
	CACCACGACC AACCATATGG CAAATGAACC AAGCCAGTT GTTGCACTGA TTGGTTGTCT	900
	TTTTCTAGAC TTGGGATCTG CAAGAAGGCC AATGCTCTAA AATTTCTGAG AACAGTGCAC	960
35	AAGATTATTT TATCACTACA AGCTTTTAAC TTTTAAAGTT ATTGTACAAG TATTCTACCT	1020
	AAATCTTCCA ATTTCTTTTA AATGGTAAGA GTTTCTAAAA CAGACAATAA TTAAACAAGC	1080
40	TCAGCTCTGC TTTATCTGAG TTTAGTGGTC CTAATATATA TGTAAGAGAA GATGGTGGGG	1140
	TTGTTACCT CTGTACAGAC CATCTGTATG TTAGGTGACA TTGATTATGG GTTATAATCA	1200
	GGGAACTAA TTGTATTTAG TGACAAAAT AAAAAGTTTT TTTTATATA TTCAGTCTGC	1260
45	TTTTGGATTT TCATATATTT AACTTTGCAA AAAGATTTAC TTTGTACATG TTACAGGCTT	1320
	GATGGTGTA AATCTTTTAA TAAATACATA AATAAAGNA AAATATGCAT TTTTCTTTTC	1380
50	TAAAAAATAA AAAAAAATAA CTCGA	1405

55 (2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1596 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

5	GTCATGCAGT GCGCCGGAGA ACTGTGCTCT TTGAGGCCGA CGCTAGGGGC CCGGAAGGGA	60
	AACTGCGAGG CGAAGGTGAC CGGGGACCGA GCATTTTCAGA TCTGCTCGGT AGACCTGGTG	120
	CACCACCACC ATGTTGGCTG CAAGGCTGGT GTGTCTCCGG ACACTACCTT CTAGGGTTTT	180
10	CCACCCAGCT TTCACCAAGG CCTCCCCTGT TGTGAAGAAT TCCATCACGA AGAATCAATG	240
	GCTGTTAACA CCTAGCAGGG AATATGCCAC CAAAACAAGA ATTGGGATCC GCGTGGGAG	300
15	AACTGGCCAA GAACTCAAAG AGGCAGCATT GGAACCATCG ATGGAAGAAA TATTTAAAT	360
	TGATCAGATG GGAAGATGGT TTGTTGCTGG AGGGGCTGCT GTTGGTCTTG GAGCATGTG	420
	CTACTATGGC TTGGGACTGT CTAATGAGAT TGGAGCTATT GAAAAGGCTG TAATTTGGCC	480
20	TCAGTATGTC AAGGATAGAA TTCATTCCAC CTATATGTAC TTAGCAGGGA GTATTGGTTT	540
	AACAGCTTTG TCTGCCATAG CAATCAGCAG AACGCTGTTC CTCATGAACT TCATGATGAG	600
25	AGGCTCTTGG GTGACAATTG GTGTGACCTT TGCAGCCATG GTTGGAGCTG GAATGCTGGT	660
	ACGATCAATA CCATATGACC AGAGCCCAGG CCCAAAGCAT CTTGCTTGGT TGCTACATTC	720
	TGGTGTGATG GGTGCAGTGG TGGCTCCTCT GACAATATTA GGGGTCCTC TTCTCATCAG	780
30	AGCTGCATGG TACACAGCTG GCATTGTGGG AGGCCTCTCC ACTGTGGCCA TGTGTGCGCC	840
	CAGTGAAGAA TTTCTGAACA TGGGTGCACC CCTGGGAGTG GGCCTGGGTC TCGTCTTTGT	900
35	GTCTTCATTG GGATCTATGT TTCTTCCACC TACCACCGTG GCTGGTGCCA CTCCTTACTC	960
	AGTGGCAATG TACGGTGGAT TAGTTCTTTT CAGCATGTTC CTTCTGTATG ATACCCAGAA	1020
	AGTAATCAAG CGTGCAGAAG TATCACCAAT GTATGGAGTT CAAAAATATG ATCCCATTA	1080
40	CTCGATGCTG AGTATCTACA TGGATACATT AAATATATTT ATGCGAGTTG CAACTATGCT	1140
	GGCAACTGGA GGCAACAGAA AGAAATGAAG TGAATCAGCT TCTGGCTTCT CTGCTACATC	1200
45	AAATATCTTG TTAAATGGGG CAGATATGCA TTAAATAGTT TGTACAAGCA GCTTTCGTTG	1260
	AAGTTTAGAA GATAAGAAAC ATGTCATCAT ATTTAAATGT TCCGGTAATG TGATGCCTCA	1320
	GGTCTGCCTT TTTTCTGGA GAATAAATGC AGTAATCCTC TCCCAAATAA GCACACACAT	1380
50	TTTCAATTCT CATGTTGAG TGATTTTAAA ATGTTTGGT GAATGTGAAA ACTAAAGTTT	1440
	GTGTCAATGAG AATGTAAGTC TTTTCTTAC TTTAAATTT AGTAGGTTCA CTGAGTAACT	1500
55	AAAATTTAGC AAACCTGTGT TTGCATATTT TTTKGGAGTG CAGMMTAWTG TAATTARAGC	1560
	ATTCCAGTAA NAGTGTNTTT AAAGTTGNTC TATATN	1596
60		

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

	GCGCAGAGCC CGYACGAGCA GGACGACGAC GACAAGGGCG ACTCCAAGGA AACGCGGCTG	60
	ACCTTGATGG AGGAAGTGCT CCTGCTGGGC CTCAAGGACC GCGARGGTTA CACATCATTT	120
15	TGGAATGACT GTATATCATC TGGATTACGT GGCTGTATGT TAATTGAATT AGCATTGAGA	180
	GGAAGGTAC AACTAGAGGC TTGTGGAATG AGACGTAAAA GTCTATTAAC AAGAAAGGTA	240
20	ATCTGTAAGT CAGATGCTCC AACAGGGGAT GTTCTTCTTG ATGAAGCTCT GAAGCATGTT	300
	AAGGAACTC AGCCTCCAGA AACGGTCCAG AACTGGATTG AATTACTTAG TGGTGAGACA	360
	TGGAATCCAT TAAAAATGCA TTATCAGTTA AGAAATGTAC GGGAACGATT AGCTAAAAAC	420
25	CTGGTGAAA AGGGTGTATT GACAACAGAG AAACAGAACT TCCTACTTTT TGACATGACA	480
	ACACATCCCC TCACCAATAA CAACATTAAG CAGCGCCTCA TCAAGAAAGT ACAGGAAGCC	540
30	GTCTTGACA AATGGGTGAA TGACCCTCAC CGCATGGACA GCGCTTGCT GGCCCTCATT	600
	TACCTGGCTC ATGCCCTCGGA CGTCTGGAG AATGCTTTTG CTCCTCTTCT GGACGAGCAG	660
	TATGATTGG CTACCAAGAG AGTGCGGCAG CTTCTCGACT TAGACCCTGA AGTGAATGT	720
35	CTGAAGGCCA ACACCAATGA GGTCTGTGG GCGGTGGTG CGGCGTTCAC CAAGTAACTC	780
	TGCTCGGGT GAACCATCTC CTTTCTCTC AAGTAAACCA GTAGTTTTTC TTCTGTGAC	840
40	TTCTGGTTTT CTGTAATTTG TACTTTCCCA CACTATAATT GGCTTCTGTT TTACAAAATG	900
	GTGGGTGGCT TTTTCTTTTT TGTACGTGTA CAGGATTCTG CTGGTACGAG AGGCCTTCCT	960
	CTTCTGTTT TTAATAAAG TTTTACTGCC ATATTGGCAT TCCATTCCCT GTTGCCATCC	1020
45	TCACTGTTAC CTGTTTGGG TTTCTGGTCT ACTTTGACTT TCAAAGTACC TCCAGCCTCC	1080
	TCATACGCAC AGCTTTTGGG TGACCTCAGC TTGAGTTTCT CCATATGTGC ATGTACATCT	1140
50	AGCATCTGC CTACAGTTCA GACAGAAGTC AAAAAAGGC CTTCAACTCA CCAAAGGTAA	1200
	ATATCTGTAT CTATTAGGAC ATTTTITACA TAGACTTCAG TTGAGATGTA TACTTAGCAA	1260
	AATTATTTTT AAATTGAAAC AGCACAGTAA ATACTTAATA TAAATGTCC CTTGGATTTT	1320
55	GCTTCCCATG TAAATCTATT GTATTATTAC ACTTGTATA ATTTTAACTA TAAAGGTCCA	1380
	ATTGTTTCAC AGAGCCAGTT TGGGATGGGC TGCATTCCAT TTATGCTGTA TATAGTTTGA	1440
60	ATTATATATA AATTACCCCT TCTTCTGGCC ACCCTGCTC CCATCTTAGT ATTTTGCAAG	1500

ATCTAATCAG TTGTACACCT GGTGCCCCCTC GCTTGCTTCA ATCATGGTTA TTTGATGGCA 1560
 5 AAATCGACCT CTTGTGCTG AAGGAGAGAG AAAAGATGTG TGTCTGATTG GTCCTGGGAT 1620
 TTTTGTAGCT GTGCCATTTA TGGTACTCTT TGCCTATGCA TCCCCTTTTT AGATTTTTTT 1680
 TAAATTTTAT CTTACTGTTT TTATAATTTT TATTGGAAG AGGCTTGTA CCAGTACCAA 1740
 10 TCTTGAGTTT CTTTTTCTGT CCACAAGTAA ATTAATATCT GCTCTGAAAT GTCATTTATC 1800
 TACTCACACA TTCTTGGGA AAAAAATCAA ATGTCAGTCC TAGCAGATGT TGCATGTAAA 1860
 TTGGTAGCAA GTAATGATTA CAACCCAGAG GATTAAGAAT TTTGTAACAG AAAGCTCTAT 1920
 15 GTTTTAATTT TTTATATACA ATTAGGATAA TTAGCATTGT CAGACTATAA ACCTTTGCTT 1980
 TTTAAAGTTT ATTTTACTA TTTCTTTATC ACTTTATTGT ATCATCACCA TTGGTTTCAT 2040
 20 AATGTAAATA CTATATGTTG AACAAATTAA ATGTCAAAAT TTTTATTAC CATAGTCCAT 2100
 GTTAATAGTG GGGCTTTCAG GTGTTTAGAG ATTTTTTTTG TTGTTGTAA CATTCAATGC 2160
 AAAAGTACTA GATGGTGTAT AACTCTAGAG TTGAATTTTA AGGGATTCCC TAATATGTAT 2220
 25 ACTATCTTTT TATCTGAAGT AATAAATAA CAATGATCTT GAAAGTGCCY RAAAMAAAAA 2280
 AAAAAAAAAA AAA 2293

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(2) INFORMATION FOR SEQ ID NO: 186:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GGCACGAGGC GAGCCGGCGC ACCGTACGCT GGGACGTGTG GTTTCAGCTC GTGCGCCTCC 60
 45 CGTGGGTTT GCGACGTTA GCGACTATTG CGCCTGCGCC ACGCCGGCTG CGAGACTGGG 120
 GCCGTGGCTG CTGGTCCCGG GTGATGCTAG GCGGCTCCCT GGGCTCCAGG CTGTGCGGG 180
 GTGTAGGTGG GAGTCAGGA CGTTTCGGGG CCCGAGGTGT CCGCGAAGGT GGCGCACATG 240
 50 GGCGGCAGGG GAGAGCATGG CTCAGCGGAT GGTCTGGGTG GACCTGGAGA TGACAGGATT 300
 GGACATTGAG AAGGACCAGA TTATGAGAT GGCTGTCTG ATAAGTACT CTGATCTCAA 360
 55 CATTTTGGCT GAAGTCTTA ACCTGATTAT AAAACAACCA GATGAGTTGC TGGACAGCAT 420
 GTCAGATTGG TGTAAGGAGC ATCACGGGAA GTCTGCGCTT ACCAAGGCAG TGAAGGAGAG 480
 TACAATTACA TTGACGAGG CAGAGTATGA ATTTCTGTCC TTTGTACGAC AGCAGACTCC 540
 60

TCCAGGGCTC TGTCCACTTG CAGGAAATTC AGTTCATGAA GATAAGAAGT TTCTTGACAA 600
 ATACATGCCC CAGTTCATGA AACATCTTCA TTATAGAATA ATTGATGTGA GCACTGTATA 660
 5 AGAACTGTGC AGACGCTGGT ATCCAGAAGA ATATGAATTT GCACCAAAGA AGGCTGCTTC 720
 TCATAGGGCA CTTGATGACA TTAGTGAAAG CATCAAAGAG CTTCAGTTTT ACCGAAATAA 780
 CATCTTCAAG AAAAAAATAG ATGAAAAGAA GAGGAAAATT ATAGAAAATG GGGAAAATGA 840
 10 GAAGACCGTG AGTTGATGCC AGTTATCATG CTGCCACTAC ATCGTTATCT GGAGGCAACT 900
 TCTGGTGGTT TTTTTTCTC ACGCTGATGG CTTGGCAGAG CACCTTCGGT TAACCTGCAT 960
 15 CTCCAGATTG ATTACTCAAG CAGACAGCAC ACGAAATACT ATTTTTCTCC TAATATGCTG 1020
 TTTCCATTAT GACACAGCAG CTCCTTTGTA AGTACCAGGT CATGTCCATC CCTTGGTACA 1080
 TATATGCATT TGCTTTTAAA CCATTCTTT TGTTTAAATA AATAAATAAG TAAATAAAGC 1140
 20 TAGTTCTATT GAAATGCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1200
 AAAAAAAAAA AN 1212

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(2) INFORMATION FOR SEQ ID NO: 187:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GCTTCCGGAA GTTGCTTTTG TCCAAACATC CGGGCTTCTC CTTTGTGTGT TCCGGCCGAT 60
 40 CCCACCTCTC CTCGACCTTG GACGTCTACC TTCCGGAGGC CCACATCTTG CCCACTCCGC 120
 GCGCGGGGCT AGCGCGGGTT TCAGCGACGG GAGCCCTCAA GGGACATGGC AACTACAGCG 180
 GCGCCGGCGG GCGCGCCCG AAATGGAGCT GGCCCGAAT GGGGAGGGTT CGAAGAAAAC 240
 45 ATCCAGGCGG GAGGCTCAGC TGTGATGAC ATGGAGAACA TGGATGATAC CTCAGGCTCT 300
 AGCTTCGAGG ATATGGGTGA GCTGCATCAG CGCCTGCGCG AGGAAGAAGT AGACGCTGAT 360
 50 GCAGCTGATG CAGCTGCTGC TGAAGAGGAG GATGGAGAGT TCCTGGGCAT GAAGGGCTTT 420
 AAGGGACAGC TGAGCCGGCA GGTGGCAGAT CAGATGTGGC AGGCTGGGAA AAGACAAGCC 480
 TCCAGGGCCT TCAGCTTGTA CGCCAACATC GACATCCTCA GACCCTACTT TGATGTGGAG 540
 55 CCTGCTCAGG TCGGAACAGG GCTCCTGGAG TCCATGATCC CTATCAAGAT GGTCAACTTC 600
 CCCCAGAAAA TTGCAGGTGA ACTCTATGGA CCTCTCATGC TGGTCTTCAC TCTGGTTGCT 660
 60 ATCCTACTCC ATGGGATGAA GACGTCTGAC ACTATTATCC GGGAGGGCAC CCTGATGGGC 720

	ACAGCCATTG GCACCTGCTT CGGCTACTGG CTGGGAGTCT CATCCTTCAT TTACTTCCTT	780
5	GCCTACCTGT GCAACGCCCA GATCACCATG CTGCAGATGT TGGCACTGCT GGGCTATGGC	840
	CTCTTTGGGC ATTGCATGT CCTGTTCATC ACCTATAATA TCCACCTCCA CGCCCTCTTC	900
	TACCTCTTCT GGCTGTGGT GGGTGGACTG TCCACACTGC GCATGGTAGC AGTGTGTGTG	960
10	TCTCGGACCG TGGGCCCCAC ACAGCGGCTG CTCCTCTGTG GCACCTTGGC TGCCCTACAC	1020
	ATGCTCTTCC TGCTCTATCT GCATTTTGCC TACCACAAAG TGGTAGAGGG GATCCTGGAC	1080
15	ACACTGGAGG GCCCCAACAT CCCGCCCATC CAGAGGGTCC CCAGAGACAT CCCTGCCATG	1140
	CTCCCTGCTG CTCGGCTTCC CACCACCGTC CTCAACGCCA CAGCCAAAGC TGTTCGGTG	1200
	ACCCTGCAGT CACACTGACC CCACCTGAAA TTCTTGGCCA GTCCTCTTTC CCGCAGCTGC	1260
20	AGAGAGGAGG AAGACTATTA AAGGACAGTC CTGATGACAT GTTTCGTAGA TGGGGTTTGC	1320
	AGCTGCCACT GAGCTGTAGC TGCCTAAGTA CCTCCTTGAT GCNTGTGGC ACTTCTGAAA	1380
25	GGCACAAGGC CAAGAACTCC TGGCCAGGAC TGCAAGGCTC TGCAGCCAAT GCAGAAAATG	1440
	GGTCAGCTCC TTTGAGAAAC CCTCCCCACC TACCCCTTCC TTCTCTTTA TCTCTCCAC	1500
	ATTGTCTTGC TAAATATAGA CTTGGTAATT AAAATGTTGA TTGAAGTCTG GAAAAAAAAA	1560
30	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAC TCGAG	1605

35 (2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

45	ATTTCGGCATG AGGGGGTCAC GTGGTGGCTG GGCCGGGGAA ATGGCGGCTT CAGGAGAGAG	60
	CGGGACTTCA GCGGCGGAG GCAGCACCGA GGAAGCATTT ATGACCTTCT ACAGTGAGGT	120
50	GAAACAAATA GAGAAGAGAG ACTCGTTTCT AACTTCGAAA AATCAGATTG AAAGACTGAC	180
	CCGTCTGGT TCCTCTTACT TCAATTTGAA CCCATTTGAG GTTCTTCAGA TAGATCCTGA	240
	AGTTACAGAT GAAGAAATAA AAAAGAGGTT TCGGCAGTTA TCCATCTTGG TGCATCCTGA	300
55	CAAAAATCAA GATGATGCTG ACAGAGCACA AAAGGCTTTT GAAGCTGTGG ACAAAGCTTA	360
	CAAGTTGCTA CTGGATCAGG AGCAAAAGAA GAGGGCCCTG GATGTAATTC AGGCAGGAAA	420
60	AGAATACGTG GAACACACTG TGAAAGAGCG AAAAAACAA TTAAAGAAGG AAGGAAAACC	480

TACAATTGTA GAGGAGGATG ATCTGAGCT GTTCAAACAA GCTGTATATA AACAGACAAT 540
GAAACTCTTT GCAGAGCTGG AAATTAAAAG GAAAGAGAGA GAAGCCAAAG AGATGCATGA 600
5 AAGGAAACGA CAAAGGGAAG AAGAGATTGA AGCTCAAGAA AAAGCCAAAC GGGAAAGAGA 660
GTGCAGAAA AACTTTGAGG AAAGTCGAGA TGGTCGTGTG GACAGCTGGC GAAACTTCCA 720
AGCCAATACG AAGGGGAAGA AAGAGAAGAA AAATCGGACC TTCTGAGAC CACCGAAAGT 780
10 AAAAATGGAG CAACGTGAGT GACCGCCCAA GGTACAGGC ACAGAACCTT TCCCCTGCTA 840
TCTCCCTTCC TGCTTCGAAG GACTCATTCT TTCCTCCAC TTCCACCCCA ACATAGAGTA 900
15 GTATTTGCTT TTTAGTCCAT TTTGTTTTCA ATACGATTTA ATATCGATCA GAGTAATTCT 960
TTTGTACATT GAAATGAGGG GCTTGGTTTA AAAAAAGACC TTTCCCTCTC CCTGCCCCCTA 1020
GAACAACCAG TATTAGAAGG TGCCACCATT GGTGCTGCCT TCTCTTCCA CAGCCTGTAA 1080
20 CTCAGTGTTT TGTACTTCAC TGAATGTGA TGGTTAGAAA CTTCGTGGAT AGTTTGTGGA 1140
AATCATCCAA TTAAACATAC TGCTTAAAC AGTGTGCTG TGACTTCAGA GACAAGCCTG 1200
25 GAAGGGGCAC CTTAGGAAGC CCCTTCGCTT CAGTTGCTCG CTTCCTGGGTG TGCTCCCTTC 1260
GAAGGCCAG ATAAGACAGG GAACACTTGT GAGCACACAG AGCAGCATCT GATGCCCTGT 1320
GGTGTMTGGC ATGTGCCCCC TGTCTACTGA CCAATCAGTG TGGCATGAGG CCCACGCCAC 1380
30 CCAAACCTTT CACTTTCCAA AGAGCTAGCC GTCCTCCACC CAGTACCATG TCCTAGCCTG 1440
TCTGCATTTG TTAGTGGTAA TATTCTTTAT GTATAATAAA TTTTATACC CAAAAAAAAA 1500
35 AAAAAAAAAA ACTCGA 1516

40 (2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50 GCTCCCATGT TGCTGGCTGT CCGTACATCA CCCTGTCCCC TGCAGGAGGG GGCTACAGGC 60
CATCTCCCTC CTGTAGGCCT CTGACTCCCC TCCACTTTTG GGCCCTCAGC TTATCTCGGG 120
CAGGGGACCA TTGCAGCATC CTCCCCTCCT CNGGACTCAA GGTGCTGAGG TATAAGCCCT 180
55 GGGCCCCAGA TCCCTGRTKA CACCTTCTCG GAGAAGACTC TCAAAAGTGA CTGTATATTT 240
GAGTTCACCA GCAATAACTC CCCACACTCG AAGCAGGTCC AAACCCMAGG ATCCCAGGGT 300
60 CCTTGGGCTC TGTGGCACTG TCTTCCCAAG ATCCTTCTCG TTGCACAATG GGAAACCTAA 360